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GenCore version 5.1.6
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- protein search, using sw model OM protein

March 9, 2004, 17:15:33 ; Search time 9.71143 Seconds Run on:

(without alignments)
2813.016 Million cell updates/sec

US-10-006-011A-9

1 CERQPCQHGATCMPAGEYEF........QPLDLQHRAQAGANTRPCPS 284 Perfect score: Sequence:

BLOSUM62 Scoring table:

283366 seqs, 96191526 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 3: pir2: \* 4: pir4: \* PIR 78:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	perlecan precursor	heparan sulfate pr	tical pro	- rat			slit-1 protein hom	hypothetical prote	cadherin-related t	hypothetical prote	protein F40E10.4 [	MEGF5 protein - ra	d leucine	laminin alpha-2 ch	neurexin III-alpha	neurexin III-alpha	neurexin III-alpha	G-cadherin - sea u	o o	notch3 protein - h	neurexin I-alpha -	hypothetical prote	neurexin I-alpha p			laminin alpha-1 ch	hypothetical prote	nju	Die 21 E
SUMMAKIES	ID	A38096	518252	T19821	AGRT	T43060	AGCH	T42218	T20721	ICEFTM	T22025	D89711	T13953	T42626	MINISTUME	A48216	B48218	148216	T30213	S53868	S7854.9	I45944	T20968	A40228	C40228	Н.	S14458	ũ	T37316	, COOOE
	DB	5												N																
	Length	4391	3707	3375	1959	1328	1955	1531	4307	5147	601	601	1523	1025	1751	1438	1471	1578	2809	3106	2321	1530	2610	1507	1715	3034	3075	3672	3704	000
d	Query Match	100.0	•		21.	7	19.3	Н	Н	Н	Н	15.9	-	15.	Н	13.	Ч	13.	13.	4	12.7	٠	•	12.5	•	12.2	12.0	11.8	11.8	, ,
	core	1566	1370.5	349	333.5	314.5	301.5	283.5	264	264	249	249	246	243.5	223.5	217	217	217	214	207.5	199	197.5	197.5	196.5	194.5	191	188.5	185.5	185.5	,0,
	Result No.	<del> </del>	2	m	4	S	9	7	00	σ	10	11	12	13	14	15	16	17		19			22	23	24	25	26	27		

slit protein 2 pre	slit protein 1 pre	notch 3 protein -	notch protein homo	notch-1 protein -	notch homolog - se	notch4 - mouse	adhesive plaque pr	hypothetical prote	Motch B protein -	cell-fate determin	notch protein homo	jagged protein pre	preadipocyte facto	homeotic protein d	neurocan - mouse	
B36665	A36665	S45306	S18188	A46019	T31070	T09059	A56175	T32934	A49175	A49128	A40043	A56136	A54785	853718	S52781	
~	~	~	N	N	N	N	N	N	N	N	7	N	~	N	N	
1469	1480	2318	2531	2531	2531	1964	473	1647	1203	2471	2555	1220	385	385	1268	
11.7	11.7	11.6	11.6	11.6	11.5	11.3	11.3	11.2	11.2	11.2	11.1	11.0	10.9	10.9	10.8	
183	183	182	181.5	181.5	180	177.5	176.5	176	175	175	174.5	173	170	170	169.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

RESULT 1

periecan precursor - numan N/Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate protec
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
R; Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A, Title: Primary structure of the human heparan sulfate proteoglycan from basement membra
tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
A; Reference number: A38096; MUID:92235084; PMID:1569102
A; Accession: A38096
A;Molecule type: mRNA
A;Residues: 1-4391 <mur></mur>
A;Cross-references: GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427
R;Kallunki, P.; Tryggyason, K.

A.Molecule type: mRNA A.Residues: 1-57, 70', 59-434, A', 436, FL', 438-449, 'Q', 451-502,'A', 503-792,'K', 794-908,'R', 71-2979,'H', 2981-294,'G', 2996-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-35, A,Cross-references: EMBL.X62515 A.Cross-references: EMBL.X62515 B.Tryggwason, K. SMBL. Data Library, October 1991 A.Reference number: S77946

A; Molecule type: mRNA A; Residues: 1-57, 10', 59-434, 7A', 436, FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R', 71-2979, 'H', 2981-2994, 'Q', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-46 A; Cross-references: EMBL: X62515; NID: 929469; PIDN: CAA44373.1, PID: 929470 B; Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K. A; Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the generate number: A41059; MUD: 92120660; PMID: 1685141 A; Accession: S77946

A; Accession: A41059

A, Molecule type: mRNA A, Molecule type: mRNA A, Residues: YT. '892-908, RK, 910-1101, 'L', 1103-1132, 'L', '1134-1221, 'L', '1223-1397 < KA2> A, Cross-references: GB:S76436; NID:9243370; PIDN:AABS1121.1; PDD:9243371 R; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F Genomics IO, 673-869, 1991 A; Pitle: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula: A, Reference number: A40306; MUID:91365376; PMID:1679749 A, Accession: A403 A, Accession: A403 A, Accession: A403 A, Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD> A, Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD> B, Heremans: A: van der Schueren, B:; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den J. Cell Biol. 109, 3199-3211, 1989

Y.; He

a basement membrane heparan sulfate proteogl

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A, Molecule type: mRNA
A;Residues: 1.3707 <NUO>
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AA33911.1; PID:g200296
B;Cross-references: EMBL:M77174; NID:g200295; PIDN:AA33911.1; PID:g200296
B;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hase
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
                     D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada,
                                                                                                                              A; Reference number: $18252; MUID: 92078153; PMID: 1744087
                                                                        The complete sequence of perlecan,
                                                                                                                                                               A;Accession: S18252
                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A31917
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                                                                                                                                                                                                                                                                                                      A/Gene: GDB.HSPG2
A/Cross-references: GDB:126372; OMIM:142461
A/Cross-references: GDB:126372; OMIM:142461
A/Map Position: 1p36.1-1p36.1
C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; Laminin G repe C;Z-121/Domain: signal sequence #status predicted <SIG>
F;22-4391/Product: perlecan #status predicted <MAT>
E;22-133/Domain: I cDOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F/3845-3880/Domain: EGF homology <EGF1>
F/3888-3921/Domain: EGF homology <EGF>
F/3953-4106/Domain: EGF homology <EGF>
F/3417-4175/Domain: EGF homology <EGF2>
F/419-4151/Region: motor neuron attachment (L-R-E) motif
F/419-4151/Region: motor neuron attachment (L-R-E) motif
F/4299-4301/Region: motor neuron attachment (L-R-E) motif
F/55/71.76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F/89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval
               core protein-specific monoclona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4228 ETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
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100.0%; Pred. No. 3.2e-105;
.ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;194-530/Domain: II <DOM2>
F;199-234/Domain: LDL receptor ligand-binding repeat homology
F;285-319/Domain: LDL receptor ligand-binding repeat homology
F;325-359/Domain: LDL receptor ligand-binding repeat homology
F;368-403/Domain: LDL receptor ligand-binding repeat homology
F;536-403/Domain: III <DOM3>
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                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 2166-2171,'X', 2173-2175,'X', 2177-2185 <HB3>
A;Note: poptide potentially matches four different regions
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F.1159-1206/Domain: laminin-type EGF-like homology <LEGS-
F.1563-1610/Domain: laminin-type EGF-like homology <EG7>
F.1613-1669/Domain: laminin-type EGF-like homology <LEGS-
F.1677-3686/Domain: laminin-type EGF-like homology <LEGS-
F.1677-2034/Domain: IV <DOM4>
F.2007-2034/Domain: transmembrane #status predicted <TRM>
A, Title: Matrix-associated heparan sulfate proteoglycan:
                                                      A;Reference number: A33625; MUID:90078352; PMID:2687294
A;Accession: B33625
A;Molecule type: protein
A;Residues: 1379-1384,'X',1386-1388,'X',1390-1398 <HE2>
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A; Molecule type: protein
A;Residues: 1272-1274, X',1276, X',1278-1279 < SCH>
C;Superfeatily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe.
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F;285-319/Domain: LDL receptor ligand-binding repeat homology < LDL3>
F;385-359/Domain: LDL receptor ligand-binding repeat homology < LDL3>
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F;386-403/Domain: LDL receptor ligand-binding repeat homology < LDL3>
F;385-3150/Domain: LDL receptor ligand-binding repeat homology < LEG9>
F;385-3150/Domain: LDL receptor ligand-binding vence to the second secon
A; Molecule type: mRNA
A; Residues: 940-1601 <NO2>
A; Residues: 940-1601 <NO2>
A; Residues: 940-1601 <NO2>
A; Accession: B31917
A; Molecule type: mRNA
A; Residues: 1870-2600 <NO3>
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A; Residues: 1870-2600 <NO3>
A; Cross-references: GB: J04055; NID: 9200300; PIDN: AAA39912.1; PID: 9200301
B; Schulze, B; Mann, K; Battistutta, R; Wiedemann, H.; Timpl, R.
A; Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A; Reference number: $66460; WUID: 95377282; PMID: 7649154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3485 PGFSGPRCQQGAGYGVVESDWHPEGSGGNDAPGQYGAYFYDNGFLGLPGNPGSFSRSLPEVP 3544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyporhetical protein ZC101.2e - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 23-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 INDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 3707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3664 FSSGITGCIKNLVLHTARPGAPPPQPLDLQHRAQAGANTRPCPS 3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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ilarity 86.3%; Pred. No. 4e-91;
Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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heparan sulfate proteoglycan - mouse NyAlternate names: perlecan C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 113-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 05-Nov-1999 C.Accession: S18252; A31917; B31917; S66460

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2; 2613/1; 2684/1; 2757/1; 2813/3; 2863/1; 2900/3; 3084/1; 3176/1; 3250/2 C; Superfamily: LR11 protein; laminin-type EGF-like homology; LDL receptor ligand-binding F; Reywords : extracellular matrix: F; Reywords: extracellular matrix: F; Reywords: extracellular matrix: F; Reywords: extracellular matrix: F; Reyso-24/Domain: LDL receptor ligand-binding repeat homology <LDL1> F; Reseptor ligand-binding repeat homology <LDL2> F; Reseptor ligand-binding repeat homology <LDL2> F; Reseptor ligand-binding repeat homology <LDL3> F; Reseptor ligand-binding repeat homology <LDL3> F; Reseptor ligand-like homology <LDC3> F; Reseptor ligand-like homology <LDC3> F; Reseptor ligand-like homology <LDC3> F; Reseptor ligand-like homology <LEG2> F; Reseptor ligand-like homology <LEG2> F; Reseptor ligand-like homology <LEG3> F; Reseptor ligand-like ligand-lik
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C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 17-Nov-2000
C.Accession: JMO399, A38856
R.Rupp, F.; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3228 RPTVQQMEDYISVGIVNGHLHFSYELGGGAAHLISEBRVDDGKEHSVRFERKGREGQMRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GDLCEHEE--NPCQLREPCLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLAWQGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 VGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGEELVSGRSPGPNVAVNAKGSVY1GGAPDVATLITGGRFSSGITGCVKNLVLHSARPGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3129 GDVYSTQEPNNIC-ANSTCGMNGQCVPRNMTHYTCECKLYYDGPTCSLFK----
                                                                                                                                                                                                                                                                                                                                                               Query Match
22.3%; Score 349; DB 2; Length 3375;
Best Local Similarity 31.2%; Pred. No. 4.5e-17;
Matches 81; Conservative 41; Mismatches 102; Indels 3
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'Molecule type: DNA
'Residues: 1-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545,'RIRVRS',155
'Cross-references: RMBL-293395, PIDN:CABO7704.1; GSPDB:GN00020; CBSP:ZC101.2b
'Experimental source: clone ZC101
'Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
enes Dev. 7, 1471-1484, 1993
'Trille: Products of the unc-52 gene in Caenorhabditis elegans are homologous to the cor', Reference number: A47648; MUD:93339574; PMID:8393416
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A;Introns: 32/1; 134/1; 225/1; 335/2; 450/3; 739/3; 830/3; 860/2; 1064/2; 1129/1; 1158/3
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A;Molecule type: DNA
A;Residues: 1-546,'P',548-2441,'R','KRKH',3369,'GN',3372-3373,'G',3375,'RLRHRRNAQNGPLSR
A;Cross-references: GB:L13458
A;Accession: B47648
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Cross-references: EMBL:293395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c
Experimental source: clone ZC101
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Cross-references: EMBL:293395; PIDN:CAB07706.1; GSPDB:GN00020; CBSP:ZC101.2a
Experimental source: clone ZC101
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Molecule type: DNA
Residues: 1-546,'P',548-1128,1290,'DFARNSPS',1299,'NSS',1303-1304,'R','RHR',1544-1545,
Cross-references: GB:L13458
                                                                                                                                                                                                                                                         ',Modecule type: DNA'
',Rosidues: 1-3375 < WILL>
',Rosidues: 1-3375 < WILL>
',Cross-references: EMBL.293375; PIDN:CAB07569.1; GSPDB:GN00020; CESP:ZC101.2e
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',Status: preliminary: translated from GB/EMBL/DDBJ
',Status: preliminary: translated from GB/EMBL/DDBJ
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',Accession: T19820
',Accession: T19820
',Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Residues: 1-546, P',548-2198,D',2290,'NAR',2294,'L',2296,'WHATE',2302-2303,'V',2305,
1, ANIV',2516-2517,'LQQG',2522,'IDG',2526,'S',2528,'SRGFHV',2535,'F' <RO2>
A,Cross-references: GB:L13458
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Molecule type: DNA
REGISTATION 1375 **MIL2>
GEORGE-references: BMBL:293395; PIDN:CAB07708.1; GSPDB:GN00020; CESP:ZC101.2e
FEXPERIMENTAL SOURCE: clone ZC101
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                                                                                                                                                                                          Accession: T19821
Status: preliminary; translated from GB/EMBL/DDBJ
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ubmitted to the EMBL Data Library, March 1997
;Reference number: Z20375
                                                                       Baynes, C.
ibmitted to the EMBL Data Library, March 1997
Reference number: 219182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
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A;Accession: 130052
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Returus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 'SHISNEIPA',1784-1795 <THO>
A;Cross-references: EMBL:100721; ND:9459665; PIDN:AAA16788.1; PID:9459666
A;Cross-references: EMBL:100721; ND:9459665; PIDN:AAA16788.1; PID:9459666
C;Comment: This protein mediates the motor neuron-induced aggregation of acetylcholine r C;Comment: Alternative splicing produces two inactive proteins: agrin-related protein 1 C;Comment: Alternative splicing; produces two inactive proteins: agrin-related proteins agrin-related protein 1 Fstatus predicted <AGG>
C;Keywords: alternative splicing; duplication; qlycoprotein; neuromuscular junction P;1-38/Domain: agrin-related protein 1 #status predicted <AGG>
F;39-1955/Product: agrin-related protein 2 #status predicted <AGG>
F;39-1647,1652-1783,1794-1955/Product: agrin-related protein 2 #status predicted <AGG>
F;39-1487,1652-1783,1794-1955/Product: agrin-related protein 2 #status predicted <AGG>
F;39-1487,1652-1783,1794-1955/Product: agrin-related protein 2 #status predicted <AGG>
F;39-1487,1652-1783,1794-1955/Product: agrin-related protein 3 #status predicted <AGG>
F;30-1487,1652-1783,1794-1955/Product: agrin-related protein 3 #status predicted <AGG>
F;30-488/Domain: Kazal proteinase inhibitor homology <AFFI>
F;30-548/Domain: Kazal protein
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A; Residues: 1-1955 <TSI>
A; Cross-references: GB: M94271; NID: G211120; PIDN: AAA48585.1; PID: G211121
A; Experimental source: brain
A; Experimental source: brain
B; R; Ruegg, M.A.; Tsim, K.W.K.; Horton, S.E.; Kroeger, S.; Escher, G.; Gensch, E.M.; McMaha
Neuron B, 691-699, 1992
Neuron B, 691-699, 1992
A; Title: The agring gene codes for a family of basal lamina proteins that differ in funct
A; Reference number: A38887; MUID: 92232298; PMID: 1314621
A; Contents: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                      115 SLPEVPETIELEV--RTSTASGLLLMQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Modecule type: mRNA
A; Residues: 1221-1647;1652-1783;1794-1955 <RU3>
A; Residues: 1221-1647;1652-1783;1794-1955 <RU3>
A; Cross-references: GBs:M9737-0
A; Note: translation of the nucleotide sequence is not complete
A; Note: translation of the nucleotide sequence is not complete
B; Thomas, W.S.; O'Dowd, D.K.; Smith, M.A.
Dev. Biol. 158, 523-535, 1993
A; Title: Developmental expression and alternative splicing of chick agrin RNA.
A; Reference number: 150692; MUID:93345745; PMID:8393816
agrin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Bate: 31.Mar.1993 #text_change 17-Nov-2000
C;Accession: UHO591; A3887; B3887; I50692
R;Tsim, K.W.K.; Ruegg, M.A.; Escher, G.; Kroeger, S.; McMahan, U.J.
Neuron 8, 677-689, 1392
A;Ttle: cDNA that encodes active agrin.
A;Rtle: cDNA that encodes
                                                                                                                                                                                                                        934 -VSDLLQKLSMEVIFLAKDPNGMIFYNGQKTD--GRG-DFVSLNLRDGYLEFKYDLGKGA
                                                                                                                                                                                                                                                                                                                                                                                  173 ARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSP----GPNVAVNAKGSVYIG
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F;675-726/Domain: laminin-type EGF-like homology «LEI»
F;729-773/Domain: laminin-type EGF-like homology «LE2»
F;801-851/Domain: Kazal proteinase inhibitor homology «KPI9»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1050 GAPDFNKFARAG--IISGFTGAIQKLSLKS 1078
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A;Residues: 1132-1783;1795-1955 <RU2>
A;Cross-references: GB:M97371
A;Accession: B38857
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                                                                               요 당
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Cypecies: Discopyge ommata
Cypate: 11-0an-2000 #text_change 17-Nov-2000
Cypate: 11-0an-2000 #sequence_revision 11-Jan-2000 #text_change 17-Nov-2000
CyAccession: T43060
RySmith, M.A.; Magill-Solc, C.; Rupp, F.; Yao, Y.M.M.; Schilling, J.W.; Snow, P.; McMaha RySmith, M.A.; Magill-Solc, C.; Rupp, F.; Yao, Y.M.M.; Schilling, J.W.; Snow, P.; McMaha RySmith, M.A.; Magill-Solc, C.; Rupp, F.; Yao, Y.M.M.; Schilling, J.W.; Snow, P.; McMaha RySmith, M.A.; Magill-Solc, Tanslated from GB/EMBL/DDBJ
A;Recession: T43060
A;Recession: T43060
A;Residues: Dreliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1328 < SMIA
A;Residues: 1-1328 SMIA
A;Residues: BMBL:LO1423; NID:g213102; PID:g213103; PIDN:AAA49224.1
C;Superfamily: agrin, EGF homology; Kazal proteinase inhibitor homology; laminin G repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1807-1959/Domain: laminin G repeat homology <LG3>
F;1807-1959/Domain: laminin G repeat homology <LG3>
F;77-116, 105-137, 711-191, 180-127, 244-263, 252-284, 316-335, 324-356, 389-408, 397-429, 454-473
F;77-116, 1483-1494, 1488-1504, 150-1515/Disulfide bonds: #status predicted
F;145, 672, 827, 957/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1503 KCECPLGRGGTFCQT-----VLETAGSR----PFLADFNGFSYLELKGLHTFER 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1444 CLPNPCHGGALCQALEAGMFLCQCPPGRFGPTCADEKSPCQ-PNPCHGAAPCRVLSSGGA 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 LVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPG----PNVAVNAKGSVYIGGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 RCLCLPGPSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 SLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSPNPCKNRGKCHMKEAEMFHCESVGEFSGPTCADKHNPCD-PNPCHQSANCMVLPEGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEROPCOHGATCMPAGEYEROCLCRDGFKGDLCEHBENPCQLREPCLHGGTCQ----GT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
21.3%; Score 333.5; DB 1; Length 1959;
Best Local Similarity 36.0%; Pred. No. 3.4e-16;
Matches 94; Conservative 28; Mismatches 108; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 37;
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20.1%; Score 314.5; DB 2; Length 1328;
Best Local Similarity 31.4%; Pred. No. 5.4e-15;
Matches 85; Conservative 44; Mismatches 105; Indels 37;
                                                                               F;46-494/Domain: Kazal proteinase inhibitor homology «KPI6»
F;511-559/Domain: Kazal proteinase inhibitor homology «KPI7»
F;540-54/Region: motor neuron attachment (L-R-E) motif
F;540-645/Domain: Mazal proteinase inhibitor homology «KPI7»
F;548-739/Domain: Laminin-type EGF-like homology «KPI8»
F;688-739/Domain: laminin-type EGF-like homology «KPI8»
F;688-992/Region: Berine/theonine-rich
F;1084-1086/Region: motor neuron attachment (L-R-E) motif
F;1147-1215/Region: motor neuron attachment (L-R-E) motif
F;124-1257/Domain: EGF homology «EGI»
F;144-1446/Domain: EGF homology «EGI»
F;1483-1515/Domain: EGF homology «EG3»
F;1555-1706/Domain: EGF homology «EG3»
F;1555-1706/Domain: EGF homology «EG3»
F;1551-1706/Domain: EGF homology «EG3»
F;1650-1959/Domain: EGF homology «EG3»
F;1611-1747/Domain: EGF homology «EG4»
F;1611-1747/Domain: EGF homology «EG3»
F;1611-1747/Domain: EGF homology «EG4»
F;1611-1747/Domain: EGF
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Region: serine/threonine-rich 4/Domain: Berine/threonine-rich 4/Domain: Berine/threonine-rich 4/Domain: Berine/threonine-rich 8/Domain: laminin G repeat homolog 1/Region: motor neuron attachment 1/Domain: EGF homology <eg2> 1/Domain: EGF homology <eg3> 1/Domain: EGF homology <eg4> 1/Domain: EGF homology <eg4> 1/Domain: BGF homology <eg4> 1/Domain: Laminin G repeat homolog &lt;-EG4 4-126,160-180,169-201,233-252,241-1500,1494-1510,1512-1521/Disulfide  74,814/Binding site: carbohydrate</eg4></eg4></eg4></eg3></eg2>	Db 1145 RPVCQCLPGFGGPECEKLSVNFVDRDTYLQFTD
Dest Local Similarity 27.1%; Fig. No. 7.15-1%; Matches 87; Conservative 38; Mismatches 108; Indels 85; Gaps 13;  Qy	RESULT B T20721 hypothetical protein F25F2.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 19-May-2000 C;Accession: T20721; T21343; T23842
OY 56 RCLCLPGFSGBRCQQSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRS 115	R;Ainscough, R. submitted to the EMBL Data Library, August 1994 A;Reference number: Z19314 A;Reference number: Z19314 A;Accession: T20721 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DML A;Residues: 1-4307 <wil></wil>
154 SIGLODGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSP 213	A; Gross references: EMBi.235662; PIDN: CAA84721.1; GSPDB:GNU0021; CESF:F25F2.2 A; Experimental source: clone F10G11 R; Ainscough, R. submitted to the EMBL Data Library, August 1994
Qy 214 GPNVAVNAKGSVYIGGAPDVATLT-GGRFSSGIIGCVKNLVLHSARPGAPPQPLD 268  DD 1648 KSRKVPHAFLNLKEPFYVGGAPDFSKLARAAAISTSFYGAVQRISIKGVPLLK 1700	A;Accession: T21343 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Ablecule type: DNA A;Docidines: 1.4377 /WTA
Qy       269 LQH-RAQAGANTRPC 282                 :                       :             Db       1701 EQHIRSAVEISTFRAHPC 1718	A;Cross-references: EMB1.235599; PIDN:CAA84661.1; GSPDB:GN00021; CESP:F25F2.2 A;Experimental source: clone F25F2 R;Sulston, J. Submitted to the EMBL Data Library, June 1994
e 16-Aug-2002	A, Reference number: 21980's A, Accession: T23842 A, Accession: T23842 A, Status: preliminary, translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-4307 <wi3> A, Residues: 1-4307 <wi3> A, Experimental source: Clone M88 C, Genetics:</wi3></wi3>
; Chara, O. multiple EGF-like motifs	A;Gene: CESP:P25F2.2 A;Gene: CESP:P25F2.2 A;Gene: CESP:P25F2.2 A;Introns: 79/3; 167/3; 251/3; 328/3; 587/3; 625/3; 737/3; 1006/1; 1190/2; 1494/2; 1770/: A;Introns: 79/3; 167/3; 251/3; 328/3; 587/3; 625/3; 737/3; 1006/1; 1190/2; 1494/2; 1770/: C;Superfamily: rat MEGF1 protein; cadherin repeat homology; EGF homology; laminin G repeir; 7;3761-3900/Domain: laminin G repeat homology <lgr></lgr>
A)Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residus: 1-1531 <nax> A;Residus: 1-1531 <nax> A;Residus: 1-1531 <nax> A;Cross-references: EMBL:AB011530; NID:g3449289; PIDN:BAA32460.1; PID:g3449290 A;Experimental source: strain Sprague-Dawley; brain C;Genetics: A;Genetics: A;Gene: MEGF4 C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r</nax></nax></nax>	Query Match Best Local Similarity 26.4%; Pred. No. 8.6e-11; Matches 81; Conservative 45; Mismatches 99; Indels 82; Gaps 13;  Qy 21 QCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQ69  Db 3670 QCLCPDGFGGKRCEVETNQCAKSPCEQWQLCIPSVHNSTYECVCPLGMEGDKCSVPS 3726
Query Match Best Local Similarity 27.9%; Pred. No. 1.1e-12; Matches 81; Conservative 48; Mismatches 92; Indels 69; Gaps 14;	
Qy 1 CERQPCQHGATCWPAGEYEFQCLCRDGFKGDLCEHEENPCOLREPCHGGTCQGT 55	
Qy 56 RCLCEPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFS 113	Qy 185 EWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRF 241

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4197 KTAISTVIAGRNIADGGWHKVTATRNGRVMSLSVAKCADSGDVCTECLPGDSSCYADEVG 4256
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-601 < WIL>
A, Coss-references: EMBL: Z69792; PIDN: CAA93668.1; GSPDB:GN00028; CESP: F40El0.4
A, Experimental source: clone F40El0
                                                                                                                                                                                                                                                                         Gaps . 19;
                                                                                                                                                                                                                                                                                                                                                                                               4056 CYSKPCRNGGSCORSPDGSSYP-CLCRPGFRGNQCESVSDSCR-PNPCLHGGLCVSLKPG 4113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 PNVAVN-AKGSVYIGG---APDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 TRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F40B10.4 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 PCENNGKCIPINGSY--SCMCSPGFTGNNCETNIDDCKNVE-CQNGGSCVDGILSYDCLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LPGFSG----EGSGGNDAPGQ---GSGHGIA---ESDWHL---EGSGGNDAPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 RPGYAGOYCEIPPMADMEYOKTDACOOSACGOGECVASONSSDFTCKCHEGFSGPSCDRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 YGAYFHDDG-FLAFPGHVFSRSLPEVPE-TIELEVRTSTASGLLLWQGVEVGEAGQGKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PCQHGATCMPA-GEYEFQCLCRDGPKGDLCEHEENPCQLREPCLHGGTC----QGTRCLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 SLPEVPETIELEVRISTASGLLLWQ-GVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 R----LVSEDPINDGEWHRVTALREGRRGSIQV----DGE---BLVSGRSP-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                  1 CEROPCOHGATCM--PAGEYEFOCLCRDGFKGDLCEHEENPCOLREPCLHGGTC----OG
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                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                             16.9%; Score 264; DB 1; Length 5147;
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                                                                                                                                                                                                                       Query Match
16.9%; Score 264; DB 1; Length 5147
Best Local Similarity 29.3%; Pred. No. 1e-10;
Matches 93; Conservative 39; Mismatches 103; Indels
   F;3954-4010/Domain: EGF homology <EG1>
F;4017-4048/Domain: EGF homology <EG2>
F;4056-4089/Domain: EGF homology <EG3>
F;4056-4127/Domain: EGF homology <EG3>
F;4596-4127/Domain: EGF homology <EG4>
F;4594-4609/Domain: transmembrane #status predicted <TMM>
F;4561-0-5147/Domain: intracellular #status predicted <ITM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Smye, R.
submitted to the EMBL Data Library, February 1996
homology <EG1>
homology <EG2>
homology <EG3>
homology <EG3>
homology <EG4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z19503
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A,Gene: CESP:F40E10.4
A,Map position: X
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Best Local S
Matches 84
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A/cose-references: FlyBase:FBgn0001075

C/Superfamily: cadherin-related tumor suppressor; cadherin repeat homology; EGF homology

C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein

C/Keywords: calcium binding; cell adhesion; duplication; transmembrane protein

E/1-35/Domain: signal sequence #status predicted <BGS-

F/36-5147/Product: cadherin-related tumor suppressor #status predicted <WAT>

F/36-5147/Product: cadherin-repeat homology <CRN>
F/36-5270/Domain: cadherin repeat homology <CRN>
F/36-483/Domain: cadherin repeat homology <CRN>
F/371-382/Domain: cadherin repeat homology <CRN>
F/391-494/Domain: cadherin repeat homology <CRN>
F/313-942/Domain: cadherin repeat homology <CRN>
F/313-942/Domain: cadherin repeat homology <CRN>
F/318-948/Domain: cadherin repeat homology <CRN>
F/318-1948/Domain: cadherin repeat homology <CRN>
F/318-1156/Domain: cadherin repeat homology <CRN>
F/318-1156/Domain: cadherin repeat homology <CRN>
F/318-1138/Domain: cadherin repeat homology <CRN>
F/318-1138/Domain: cadherin repeat homology <CRN>
F/318-1384/Domain: cadherin repeat homology <CRN>
F/318-1384/Doma
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Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, C.S. ell 67, 853-868, 1991

Afther The fat tumor suppressor gene in Drosophila encodes a novel member of the cadhe Reference number: A41087; MUID:92069752; PMID:1959133
                                                                                                                                                                                                                                                                                                                                                                                                                                              cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
      3816 QWHRIAISRRQRRTRWIYDDEDLQEAFSPIGSTVINLHRYSQKLVLG-----AKVDDGEL 3870
                                                                                                                                                SSGITGCVK----AQAGAN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997 C;Accession: A41087; B41087
R;Mahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <660>
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A;Cross-references: GB:M80537
A;Note: 1229-Gly and 1233-Ser were also found
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F,1925-2027/Domain: cadherin repeat
F,2028-2167/Domain: cadherin repeat
F,2169-2278/Domain: cadherin repeat
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A;Residues: 143-485;1279-5147 <MAH>
A;Cross-references: GB:M80537
A;Accession: B41087
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F;2494-2596/Domain:
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A;Status: preliminary; translated from GB/EWBL/DDBJ A;Molecule type: mRNA A;Molecule typ	RESULT 13  T4266   secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)  NiAlternate names: neurogenic extracellular slit protein Cipaceis was musculus (house mouse) Cipate: 11-Jan-2000 #text_change 16-Aug-2002 Riblomes, G.P.; Negus, K; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.H. Mech. Dev. 79, 5-72, 1996 A; Title: Distinct but overlapping expression patterns of two vertebrate slit homologs implicates in the constant of the constant	QY         41
Db 347 VSAELYDGRVKLVYYIGNFPASHWYSSVKVNDGLPHRISIRTSERKCFLQIDKNPVQIVE 406  Qy 210 GRSPGPNVANAKGSVYIGGAPDVAILIGGRFSSGITGCVKNLVLHSARPGAPPP 264  Db 407 NSGKSDQLITKGREMLYIGGAPDVAILIGGRFSSGITGCVKNLVLHSARPGAPPP 264  QY 265 QPLDLQHAQAGANT 279  Db 460 -PINLQ-QALENVNT 472  RESULT 11  D89711  D89711  RSULT 11  D89712  RESULT 11  D89711  RSULT 11  RSULT 11  RSULT 11  D89711  RSULT 11  RSULT 11  D89711  RSULT 11  RSULT 1	Query Match         15.9%; Score 249; DB 2; Length 601;           Best Local Similarity 26.7%; Pred; No. 1.3e-10;         Length 601;           Matches 84; Conservative 48; Mismatches 115; Indels 68; Gaps 17;           QY         SPCQHGATCMPA-GEYEFQCLCRDERENPCQLREPCLHGGTCQGTRCLC 59           Pission 1   1   1   1   1   1   1   1   1   1	RESULT 12 T13953 MEGF5 protein - rat NAIternate names: slit protein homolog NAIternate names: slit protein homolog NAIternate names: slit protein homolog Cispecias: Ratus norvegicus (Norway rat) Cispecias: Ratus norvegicus (Norway rat) Cispecias: Ratus norvegicus (Norway rat) Cispecias: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002 Cispecias: Norwayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Rivarayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

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59; Conservative 23; Mismatches 67; Indels 13; Gaps
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A Molecule type: mRNA
A; Residues: 1-1368,1372-1438 <US2>
A; Cross-references: GB:L14851
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A;Molecule type: mRNA
A;Residues: 1-1438 <USH>
A;Cross-references: GB:L14851
A;Accession: B48216
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Na Alternate names: laminin M chain; merosin heavy chain

C. Date: 30-Sep-1931 #Sequence_revision 21-Aug-1998 #text_change 10-Dec-1999

C. Date: 30-Sep-1931 #Sequence_revision 21-Aug-1998 #text_change 10-Dec-1999

C. Date: 30-Sep-1931 #Sequence_revision 21-Aug-1998 #text_change 10-Dec-1999

C. Accession: No. 2122-1219, 1998

A. Michael Indian laminin M chain: Epitope analysis of its monoclonal antibodies by immunos A. Residues: 11-751 + GAS

A. Molecule type: mRNA

A. Residues: 11-751 + GAS

A. Molecule type: mRNA

A. Residues: 11-751 + GAS

A. Molecule type: mRNA

A. Residues: 11-751 + GAS

A. Molecule type: mRNA

A. Molecule to the mRNA

A. M
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C;Comment: This protein is a prominent component of the basement membrane that mediates
C;Comment: This protein is a prominent component of the basement membrane that mediates
C;Comment: This protein is a prominent component of the basement membrane that mediates
A;Gens: GDB:LAMA2; LAWM
A;Cross-references: EMBL:32362; OMIM:156225
A;Map position: Gq22-6q23
C;Complex: Lamining are trimers of an alpha-type, a beta-type, and a gamma-type laminin C;Punction:
C;Punction:
A;Description: interact with cells and with other basement membrane proteins to promote C;Superfamily: laminin alpha-1 chain; laminin Grepeat homology; laminin-type EGF-like homology *LE02-
C;Superfamily: laminin-type EGF-like homology *LE02-
F;11-165/Domain: laminin-type EGF-like homology *LE03-
F;110-165/Domain: laminin-type EGF-like homology *LE04-
F;27-567,107-1300/Region: 3DM and 2D9 binding
F;811-155/Domain: laminin Grepeat homology *LG3-
F;1191-1155/Domain: laminin Grepeat homology *LG3-
F;1191-1155/Domain: laminin Grepeat homology *LG3-
F;110-1155/Domain: laminin Grepeat homology *LG3-
F;110-1155/Domain: laminin Grepeat homology *LG3-
F;110-138,255,341,451,542,557,561,658,669,686,767,881,1001,1076,1119,1192,1199,1289,1509
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A;Molecule type: mRNA
A;Residues: 'V', 623-1264,'R', 1266-1751 <LEI>
A;Residues: 'V', 623-1264,'R', 1266-1751 <LEI>
C;Comment: This protein is a prominent component of the basement membrane that mediates
                                                                                                                                                                                             743 TLDSSLSLSVDGGSPKVITNLS--KQSTLNFDSPLYVGGMPGKNNVASLRQAPGQNGTSF 800
134 GLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLV-SEDPINDGEWHRVTAL 192
                                                                                                                                                    193 REGRRGSIQVDG--EELVSGRSPGPNVAVNAKGSVYIGGAP---DVATL--TGGRFSSGI
                                             Score 223.5; DB 1; Length 1751;
Pred. No. 2,9e-08;
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801 HGCIRNLYINS 811
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component; duplication; extracellu
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R;Ushkaryov, Y.A.; Suedhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and
A;Reference number: A48216; MUID:93342001; PMID:8341647
, 6;
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                                                                                                     122 TIELEVRISTASGILLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPI 181
                                                                                                                                                                                                                                                              182 NDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVA--VNAKGSVYIGGAP-DVATLTG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 GGTLCSEDVSQGPGLSHLMMSEQGRSKAREENVATFRGSEYLCY--DLSQNPIQSSSDEI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TLSFKTWQRNGLIL------HTGKSADYVNLALKDGAVSLVINLGSGAFEAIVE-PVNG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 KFNDNAMHDVKVTRNLRQVTISVDGILTTTGYTQEDYTMLGSDDFFYVGGSPSTADLPGS 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 GFKGLMLDLKYGNSEPRLLGSQSVQLEAEGPCGER-PCENGGICFLLDGHPTCDCSTTGY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 SGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 ELEVRISTASGLILMOGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPI-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 --NDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GFKGDLCE-----GTRCLC-LPENPCQLREPCLHGGTC----QGTRCLC-LPGF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurexin III-alpha secreted type 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%; Score 217; DB 2; Length 1438; 26.4%; Pred. No. 6.9e-08; ative 35; Mismatches 114; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1541 GPVTYSIDGCVRN--LHMAEAPADLEQPTSSFHVGTCFANAQ 1580
                                                                                                                                                                                                                                                                                                                                                                                                                  239 GRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface
F;1-Z7/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:19:08; Search time 20.844 Seconds (without alignments) 2876.963 Million cell updates/sec

US-10-006-011A-9

Title:

1 CEROPCOHGATCMPAGEYEF......OPLDLQHRAQAGANTRPCPS 284 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

809742 segs, 211153259 residues Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Published Applications AA:\*

/ CGROZ 6/ptodata/1/pubpaa/USGO/ PUBCOMB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO/ NEW PUB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO NEW PUB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO NEW PUB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO PUBCOMB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/DSGO NEW PUB.pep:\*
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/ CGROZ 6/ptodata/1/pubpaa/USGO NEW PUB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO PUBCOMB.pep:\*
/ CGROZ 6/ptodata/1/pubpaa/USGO NEW PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	US-10-094-886-180 Sequence 180, App	15-09-764-853-758 Sequence 758, App	Sequence 252,	US-09-764-881-158 Sequence 158,		US-10-242-747-158 Sequence 158,	178-249-10 Sequence 10, Appl		US-09-764-898-179 Sequence 179, App	Sequence 102,	Sequence 78,	Sequence	3 Sequence 3058	3 Sequence	****
Ð	US-10-	US-09-7	US-09-7	-60-SD	US-10-	US-10-	US-09-9	US-09-7	US-09-7	-60-SN	US-10-	US-10-	US-10-	US-10-	
DB	15	σ	σ	10	14	15	6	σ	σ	10	14	15	15	15	1
% Query Match Length DB	1931	238	238	238	238	238	375	432	432	432	432	432	463	775	
% Query Match	22.8	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	
Score	357.5	343	343	343	343	343	343	343	343	343	343	343	343	343	
Result No.	-	7	m	4	ß	9	1	œ	o,	10	11	12	13	14	

34, 28, 27,	Sequence 25, Appl Sequence 36, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl	e 432, e 333, e 333(	5696 5696 5706 31, 22, 7	Sequence 67, Appl Sequence 537, App Sequence 537, App Sequence 6999, Ap Sequence 9, Appli Sequence 396, Appli Sequence 396, Appli
-10-016-283 -10-016-283 -10-016-283 -10-016-283	3 US-10-016-283-2 3 US-10-016-283-3 0 US-09-866-050A- 3 US-10-016-283-3 1 US-09-970-944-3	1 US-10-125-540-4 1 US-09-970-944-2 1 US-10-104-044-2 5 US-10-104-047-3	5 US-10-369-493-5 5 US-10-369-493-5 5 US-10-369-493-5 3 US-10-016-283-3 4 US-10-289-76-2 0 US-09-76-511B-	4 410404
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333 330 330 330 330	330 330 330 330 330 300 300 300 300 300	283.52 283.52 278.55 269.55	264 264 264 253 253 253 253 253 253 253	25 25 25 25 25 25 25 25 25 25 25 25 25 2
114 114 118 118	122222 12222	300879	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	W 4 4 4 4 4 O C H G W 4 C

### ALIGNMENTS

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Sequence 180, Application US/10094886
Publication No. US20040002120A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
                                                                        Tchernev, Velizar T.
Liu, Xiaohong
Spytek, Kimberly A.
Patturajan, Meera
Burgess, Catherine
Vernet, Corine A.
                                                                                                                                                                                                  Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
                                                                                                                                                                                     Gorman, Linda
US-10-094-886-180
                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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Shenoy, Suresh Padigaru, Muralidhara Taupier, Raymond J., Jr. Miller, Charles Casman, Stacie Fernandes, Elma Shimkets, Richard Rastelli, Luca Spaderna, Steven Smithson, Glennda Zerhusen, Bryan Gerlach, Valerie Pochart, Pascal Pena, Carol Gangolli, Esha Gusev, Vladimir APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT

THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD APPLICANT: LARCchelle, William APPLICANT: Zhong, Mei TITLE OF INVENTION: THERAPEUTIC POLYPEPTID FILE REFERENCE: 21402-290 B CURRENT APPLICATION NUMBER: US/10/094,886

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166 GARTGKSPGMARQLNINGALYVGGMKEIALHTNRQYMRGLVGCISHFTLST-----DY 218
                                                                      ; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSGKITVDDY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GARTGKSPGMARQININGALYVGGMKEIALHTURQYMRGLVGCISHFTLST-----DY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 EIPOFIGRSYLTYDNPDILKRVSG---SRS-----NVFMRFKTTAKDGLLLWRG--DSP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AGGGKDFISLGLODGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-898-252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 EHEENPCQLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN : 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 EHBENPCOLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
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21.9%; Score 343; DB 9; Length 238;
Best Local Similarity 33.5%; Pred. No. 3.1e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: D4201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application date removed - consult PALM or file wrapper
NUMBER OF SEC ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                               ch 21.9%; Score 343; DB 9; Length 238; I. Similarity 33.5%; Pred. No. 3.1e-22; B6; Conservative 34; Mismatches 97; Indels
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; Patent No. US20020090673A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 HISLVEDAVDGKNINTC 235
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
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US-09-764-898-252
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LENGTH: 238
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CURRENT FILING DATE: 2002-03-07
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-08-17
FRICK PLING DATE: 2001-08-07
FRICK PLING DATE: 2001-08-02
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-03-08
FRICK APPLICATION NUMBER: 60/214,281
FRICK APPLICATION NUMBER: 60/214,018
FRICK APPLICATION NUMBER: 60/214,018
FRICK PLING DATE: 2001-03-08
FRICK PLING DATE: 2001-03-09
FRICK FLING DATE: 2001-03-09
FRICK APPLICATION NUMBER: 60/296,693
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: P2206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 758
LENGTH: 238
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ORGANISM: Homo sapiens
FEATURE:
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US-10-094-886-180
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US-09-764-853-758
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266 PLDLQHRAQAGANTRPC 282
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Best Local Similarity
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1 Similarity 33.5%; Pred. No. 3.1e-22;
86; Conservative 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 158
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Publication No. US20030044904A1
GENERAL INFORMATION:
APPLICATION: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REFERENCE: PUSO9C1
CURRENT APPLICATION NUMBER: US/10/073,865
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEC 1D NOS: 154
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                         Sequence 158, Application US/09764881; Publication No. US20030125246A9; GENERAL INFORMATION:
266 PLDLQHRAQAGANTRPC 282
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ORGANISM: Homo sapiens
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LOCATION: (5)
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-764-881-158
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US-10-073-865-121
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LENGTH: 238
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-073-865-121
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                                                                                                                                                                                                                               Query Match
21.9%; Score 343; DB 14; Length 238;
Best Local Similarity 33.5%; Pred. No. 3.1e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
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SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT207C1
CURRENT APPLICATION NUMBER: US/10/242,747
CURRENT FILING DATE: 2002-09-13
PRIOR PILING DATE: 2001-01-17
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PRIOR FILING DATE: 2000-01-31
PRIOR PEDICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-01-34
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-06-38
PRIOR PILING DATE: 2000-06-18
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-16
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-11
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Publication No. US20040005577A1
GENERAL INFORMATION:
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300 MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSGKITVDDY 359
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Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: P0206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ 1D NOS: 939
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
21.9%; Score 343; DB 9; Length 432
Best Local Similarity 33.5%; Pred. No. 6.6e-22;
Matches 86; Conservative 34; Mismatches 97; Indels
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Patent No. US20020090673A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-764-853-541
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LENGTH: 432
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LENGTH: 432
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Patent No. US2002010678041
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICART: Fiscella, et al.
TITLE OF INVENTION: Extracellular Matrix Polynucleotides, Polypeptides, and Antibodie
TITLE OF INVENTION WHABER: US/09/978,249
CURRENT APPLICATION NUMBER: US/09/978,249
PRIOR APPLICATION NUMBER: 60/198,123
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
SEQ ID NO 10
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                                                                                                                                                90 DAP--:-GQYGAYPHDDGFLAPPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE 145
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                                                    34 EHEENPÇQLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
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                                                                                                 11 ENAAHPC-VRAPCAHGGSCRPRKEGYDCDCPLGFEGLHCQKAIIEAI-------
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21.9%; Score 343; DB 9; Length 375;
Best Local Similarity 33.5%; Pred. No. 5.5e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
       86; Conservative 34; Mismatches 97; Indels 40; Gaps
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US-09-978-249-10
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US-09-764-853-541
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US-09-978-249-10
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies CILE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEC 1D NOS: 311
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.9%; Score 343; DB 9; Length 432; Best Local Similarity 33.5%; Pred. No. 6.6e-22; Matches 86; Conservative 34; Mismatches 97; Indels '
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; Sequence 541, Application US/09764853

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Query Match
21.9%; Score 343; DB 14; Length 432;
Best Local Similarity 33.5%; Pred. NO. 6.66-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
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US-10-242-747-102
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US-10-242-747-102
       US-10-073-865-78
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                                                                  206 BLVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQ 265
                                                                                               360 GARTGKSPGMMRQININGALYVGGMXEIALHTNRQYMRGLVGCISHFTLST-----DY 412
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21.9%; Score 343; DB 10; Length 432;
Best Local Similarity 33.5%; Pred. No. 6.6e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/09764881

Publication No. US20030125246A9

GENERAL INFORMATION:

APPLICANT: Rosen et al.

FILE REPERENCE: PT207

CURRENT APPLICATION NUMBER: US/09/764,881

CURRENT PILING DATE: 2001-01-17

CURRENT PILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 192

SOFTWARE: Patentin Ver. 2.0

SSEQ ID NO 102
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PJZ09C1
CURRENT APPLICATION NUMBER: US/10/073,865
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper or Palm NUMBER OF SEQ ID NOS: 154
SEQ ID NO 78
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CRGANISM: Homo sapiens
US-09-764-881-102
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ORGANISM: Homo sapiens
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US-09-764-881-102
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US-10-073-865-78
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90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
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34 EHEBNPCQLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
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FITTLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FITTLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PTZ0710N NUMBER: US/10/242,747
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-21
PRIOR PELICATION NUMBER: 60/180,628
PRIOR PELICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-18
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR PELING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SEC ID NO 10-21 DATE: 200
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Best Local Similarity 33.5%; Pred. No. 6.6e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
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NUMBER OF SEQ ID NOS: 5458 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4433 LENGTH: 775

TYPE: PRT

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                                                                           251 EIPQFIGRSYLTYDNPDILKRVSG~--SRS-----NVFWRFKTTAKDGLLLWRG--DSP 299
                                                                                                                                                                                                                                                                           300 MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSGKITVDDY 359
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90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
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21.9%; Score 343; DB 15; Length 463;
Best Local Similarity 33.5%; Pred. No. 7.2e-22;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
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; Publication No. US2030236392A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; FILE NO 3058
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| Publication No. US20040005560A1
| GENERAL INFORMATION:
| APPLICATI'S RESERVENT INSTITUTE
| TILLE OF INVENTION: No. US20040005560A1e1 full length cDNA
| FILE REFERENCE: HI-A0106
| CURRENT APPLICATION WHORER: US/10/108,260A
| CURRENT FILING DATE: 2002-03-27
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; ORGANISM: Homo sapiens
US-10-104-047-3058
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US-10-108-260A-4433
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; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-2933
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                                                                       Query Match
21.9%; Score 343; DB 15; Length 775;
Best Local Similarity 33.5%; Pred. No. 1.4e-21;
Matches 86; Conservative 34; Mismatches 97; Indels 40
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILTE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR PLING DATE: 2001-06-07
PRIOR PLING DATE: 2001-06-07
PRIOR PLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
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; ORGANISM: Homo sapiens
US-10-108-260A-4433
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NAME/KEY: MISC_FEATURE
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 99; Conserva
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US-10-264-049-2933
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LENGTH: 406
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101 CGRRPRVLGESPVPHTVLNLKEPLYVGGAPDFSKLARAAAVSSGFDGAIQLVSLGGRQLL 160
                                                          76 IAESDWHLEGSGGNDAPGQYGAYPHDDGFLAFPGHVFSRSLPEVPET-----IELEV 127
                                                                                                                                             218 -----VEKSAG------DVDTLAFDGRTFVEYLNAVTESEKALQSNHFELSL 258
                                                                                                                                                                                128 RISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWH 187
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375 VGCLRDVVVGR------HPLHLLBDAVTKPELRPCPT 405
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Search completed: March 9, 2004, 17:25:15 Job time: 21.844 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:16:23 ; Search time 11.1326 Seconds (without alignments) 1317.011 Million cell updates/sec

US-10-006-011A-9 1566 Title:

Perfect score:

1 CEROPCOHGATCMPAGEYEF......OPLDLOHRAQAGANTRPCPS 284 BLOSUM62 Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/GCOMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued\_Patents\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	, Appl	Appl		Appl		Appl					Appl	Appli	Appli	Appli	Appli	Appli	Appli	6, App	Appli	.83, App	3, App	Appli	App1i	444158	App1i	Appli
Ę.	30,	34	53	28	27	56	25	32	36	30	31	7	7	7	ດັ	6	6	m	N	Н	М	7	7	ž	œ	4
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Segnence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Patent No	Sequence	Sequence
ID	-08-644-	-077-		US-09-077-955-28	-09-077-955-	US-09-077-955-26	US-09-077-955-25	-08-644-271-3	US-09-077-955-36	-09-077	US-09-077-955-31	-09 - 191	US-09-540-245A-2	-60-	US-09-191-647~9	-60-	-09-540-	US-09-312-283C-396	US-09-182-024A-2	-283C-1	US-09-188-930-183	US-08-460-309-2	-08-125-	5444158-2	US-09-562-702A-8	US-09-562-702A-4
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Query Match	23	21.3	21.1	21.1	н	21.1	21.1	21.1	21.1	20.8	16.7	16.2	16.2		15.9	15.9			15.3		14.5		14,3	14.3	•	14.3
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US-09-562-702A-6	19B-7	9-4	7-4	US-09-562-702A-12	US-09-562-702A-10	2A-2	2A-4	7-5	5A-5	3-5	2-2	9-5	7-5	7-7	US-09-540-245A-7	3-7	55-2	
2-70	1-70	0-30	5-07	2-70	2-70	1-84	1-84	1-64	0-24	0-15	9-0	-3	5-07	1-64	0-24	0-15	-090	
9-56	9-26	3-46	3-12	9-26	9-56	16-6	9-91	9-19	9-54	9-54	3-23	3-46	3-12	9-19	9-54	1-54	1881	
US-0	US-09-561-709B-	US-08-460-309-4	US-08-125-077-	us-0	US-05	US-09-911-842A-	US-09-911-842A-	US-09-191-647-	0S-05	US-09-540-153-	US-09-230-652-	US-08-460-309-	US-08-125-077	US-09-191-647-	0S-05	US-09-540-153-	PCT-US91-09055-	
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28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43 .	44	4.5	

### ALIGNMENTS

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Sequence 30, Application US/08644271
Fatent No. 5814478
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS: 32
CORRESPONDENCE ADDRESS: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                       ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1996
CLASSIFTCATION 0435
PRIOR APPLICATION DATA:
FILING DATE: 15-DEC-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 195A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INPORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 1940 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: Rat Agrin

; LOCATION: 1...1940

; OTHER INFORMATION:

US-08-644-271-30
US-08-644-271-30
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Query Match

21.3%; Score 333.5; DB 2; Length 1940;

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1604 IRSKEPIALGIWVRVFLERNGRKGALQVGDGPRVLGESPKSRKVPHTMINLKEPLYIGGA 1663
                                                                                                                     1444 CLPNPCHGGALCQALEAGMFLCQCPPGRFGPTCADEKSPCQ-PNPCHGAAPCRVLSSGGA 1502
                                                                                                                                                                                                                                          1503 KČEČPLĞRSĞTFCÇT-----VLETAĞSR----PFLADFNGFSYLELKĞLHTFER 1547
                                                                                                                                                                                                                                                                                                                            1444 CLPNPCHGGALCQALEACMFLCQCPPGRFGPTCADEKSPCQ-PNPCHGAAPCRVLSSGGA 1502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 36.0%; Pred. No. 9.2e-22;
Matches 94; Conservative 28; Mismatches 108; Indels 31; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 SLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 LVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPG----PNVAVNAKGSVYIGGA 230
                                                                                                                                                                                                                                                                                                                                                                                                        175 LVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPG----PNVAVNAKGSVYIGGA 230
                                                                                                                                                                                        56 RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGGYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                                                                                                                                                                                                                  115 SLPEVPETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEAR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CEROPCOHGATCMPAGEYEFQCLCRDGFKGDLCEHBENPCQLREPCLHGGTCQ-----GT 55
                                                                                  1 CERQPCQHGATCMPAGEYZPQCLCRDGFKGDLCEHBENPCQLREPCLHGGTCQ----GT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.3%; Score 333.5; DB 4; Length 1940;
Best Local Similarity 36.0%; Pred. No. 9.2e-22;
Matches 94; Conservative 28; Mismatches 108; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JETUTANT: VALENTIALUM:
TITLE OF INVENTIALUM: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REPERENCE: REG195-8-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-12-15
EARLIER POPERIOR NUMBER: 60/008,657
EARLIER POPERIOR NUMBER: 60/008,657
EARLIER POPERIOR NUMBER: 60/008,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 34, Application US/09077955A; Patent No. 6413740; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 PDVATLT-GGRFSSGITGCVK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Rattus sp.
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LENGTH: 1940
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85 GSGGNDAPGOYGAYFHDDGFLAPPGHVFSRSLPEVPET-------IELEVR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TEATQGLVLWS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 VTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLIGGRFSSGIT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 TSTASGLLIWOGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 VVÁHREQREGSLÓVGNEAPVTGSSPLGATQLDTDGALWLGGLPELPVGPALPKAYGTGFV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 DLCEHEENPCOLR--EPCLHGGTCOGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 DVISFAGHPCIRASGHPCLNGASCVPREAAYVCLCPGGFSGPHCEKGL-----VE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 21.1%; Score 330; DB 4; Length 294;
1 Similarity 31.3%; Pred. No. 1.5e-22;
87; Conservative 34; Mismatches 99; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERENEAL INFORMATION:
APPLICANT: Valenzuela et al., David M.
APPLICANT: Valenzuela et al., David M.
APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TILE REFERENCE: REG195—28-PCT-US
CURRENT FILING DATE: 1996-09-10
EARLIER APPLICATION NUMBER: DCT/US96/20696
REALIER PILING DATE: 1996-12-13
EARLIER PILING DATE: 1996-05-10
EARLIER PILING DATE: 1996-05-10
EARLIER PILING DATE: 1996-12-15
NUMBER OF SEQ ID NOS: 36
SEQ ID NOS: 36
LENGTH: 338
LENGTH: 338
                                                                                                                             APPLICANT: Valentuela et al., David M.

TITLE OF INTENTION: NOVEL TYROSTINE KINASE RECEPTORS AND LIGANDS
FILE REPRENCE: REG195-B-DCT-US
CURRENT APPLICATION NUMBER: US/09/07/955A
CURRENT APPLICATION NUMBER: US/09/07/0566
EARLIER PELLING DATE: 1996-10
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER APPLICATION NUMBER: 09/008,657
EARLIER APPLICATION NUMBER: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 GCLRDWWGR-----HPLHLLEDAVTKPELRPCPT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 GCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 284
                                             Sequence 29, Application US/09077955A Patent No. 6413740 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09077955A Patent No. 6413740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-077-955-29
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US-09-077-955-28
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RESULT 3
US-09-077-955-29
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8
                                                                                           244 TEATQGLVLMS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLR 299
                                                                                                                                         85 GSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET------IELEVR 128
                                                                                                                                                                                                              129 ISTASGLLLWOGVEVGEAGOGKDFISLGLODGHLVFRYQLGSGEARLVSEDPINDGEWHR 188
                                                                                                                                                                                                                                  192 TEATQCLVLWS----GKATERADYVALALVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLR 247
                                                                                                                                                                                                                                                                                   189 VTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLTGGRRSSGIT 246
                                                                                                                                                                                                                                                                                                       85 GSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET-------IELEVR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 KSAG------DVDTLAFDGRTFVEYLNAVTESELANEIPVEKALQSNHFELSLR 243
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                                                                                                                                                                            144 KSAG-----DVDTLAFDGRTFVEYLNAVTESELANEIPVEKALQSNHFELSLR 191
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                                                                    31 DLCEHEENPCOLR--EPCLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLE 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 21.1%; Score 330; DB 4; Length 338; Local Similarity 31.3%; Pred. No. 1.9e-22; Nes 87; Conservative 34; Mismatches 99; Indels E
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Patent No. 6413740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-077-955-27
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Best Local Similarity
Matches 87; Conserva
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LENGTH: 390
TYPE: PRT
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US-09-077-955-27
Query Match
Best Local S
                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 KSAG-------DVDTLAFDGRTFVEYLNAVTESELANEIPVEKALQSNHFELSLR 293
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Best Local Similarity 31.3%; Pred. No. 2.7e-22;
Matches 87; Conservative 34; Mismatches 99; Indels 58; Gaps
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APPLICANT: Valenzuela et al., David M.

APPLICANT: Valenzuela et al., David M.

ITILE OF INVENTION: NOVEL TYCOSINE KINASE RECEPTORS AND LIGANDS

TILE OF INVENTION NUMBER: US/09/077,955A

CURRENT FILING DATE: 1996-09-10

EARLIER APPLICATION NUMBER: PCT/US96/20696

EARLIER APPLICATION NUMBER: 08/644,271

EARLIER PILING DATE: 1996-05-10

EARLIER FILING DATE: 1996-05-10
                                                                                                                                   APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LICANDS
FILE REPERENCE: REG195-8-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER PILING DATE: 1996-05-10
EARLIER PLING DATE: 1996-05-10
EARLIER PLING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
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                                                     Sequence 26, Application US/09077955A Patent No. 6413740 GENERAL INFORMATION:
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SEQ ID NO 25
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US-09-077-955-26
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; ORGANISM: Homo sapiens
US-09-077-955-25
RESULT 6
JS-09-077-955-26
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LENGTH: 440
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247 GCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 284
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US-09-077-955-36
OTHER INFORMATION:
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US-08-644-271-32
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                                                                                                                                                                                         129 TSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHR 188
                                                                                                                                                                                                          189 VTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGIT 246
                                                                      31 DLCEHBENPCQLR--EPCLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLE 84
           Query Match
21.1%; Score 330; DB 4; Length 456;
Best Local Similarity 31.3%; Pred. No. 2.8e-22;
Matches 87; Conservative 34; Mismatches 99; Indels 58; Gaps
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILICATION NUMBER: US/08/644,271
FILICATION DATA:
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REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 492 amino acids TYPE: amino acid amino acid
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LOCATION: 1...492
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85 GSGGNDAPGQYGAYFHDDGFLAFPGHVPSRSLPEVPET--------IELEVR 128
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                                                                                  58; Gaps
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21.1%; Score 330; DB 4; Length 492;
Best Local Similarity 31.3%; Pred. No. 3.1e-22;
Matches 87; Conservative 34; Mismatches 99; Indels 58; Gaps
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Sequence 36, Application US/09077955A

GENERAL INFORMATION:

APPLICANT: Valenzuela et al., David M.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS

TITLE REFERENCE: REG195-B-PCT-US

CURRENT APPLICATION NUMBER: US/09/077,955A

CURRENT APPLICATION NUMBER: PCT/US96/20696

EARLIER APPLICATION NUMBER: 08/644,271

EARLIER FILING DATE: 1996-05-10

EARLIER FILING DATE: 1996-05-10

EARLIER PILING DATE: 1996-05-10

EARLIER PILING DATE: 1995-12-13

NUMBER: OF SEQ ID NOS: 36

SOFTWARE: PATENTIN VOY: 2.0
Query Match 21.1%; Score 330; DB 2; Length 492; Best Local Similarity 31.3%; Pred. No. 3.1e-22; Matches 87; Conservative 34; Mismatches 99; Indels
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; TYPE: PRT ; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 DDGFLAFPGHVFSRSLPEVPET------IELEVRTSTASGLLLWQGVEVG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 EELVSGRSFGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITGCVKNLVLHSARFGAP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 EAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 PCLNGASCVPREAAYVCLCPGGPSGPHCEKGL------VEKSAG------- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
20.8%; Score 326; DB 4; Length 256;
Best Local Similarity 32.1%; Pred. No. 3e-22;
Matches 84; Conservative 32; Mismatches 90; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ## Sequence 31, Application Us/09077955A
| Patent No. 6413740|
| GENERAL INPORMATION:
| APPLICANT: Valenzuela et al., David M. APPLICANT: Valenzuela et al., David M. ITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS |
| TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS |
| FILE REFERENCE: REG195-B-PCT-US |
| CURRENT APPLICATION NUMBER: US/09/077,955A |
| CURRENT APPLICATION NUMBER: PCT/US96/20696 |
| EARLIER APPLICATION NUMBER: 08/44,271 |
| EARLIER PILING DATE: 1996-12-13 |
| EARLIER PILING DATE: 1995-12-15 |
| NUMBER OF SEQ ID NOS: 36 |
| SOFTWARE: PatentIn Ver: 2.0 |
| SEQ ID NO 31 |
| LENGTH: 216
                                                                                                                                                                                APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TITLE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-15-10
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER APPLICATION NUMBER: 2.0
263 PPQPLDLQHRAQAGANTRPCPS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 --HPLHLLEDAVTKPELRPCPT 255
                                                                                                                     ; Sequence 30, Application US/09077955A; Patent No. 6413740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 30
LENGTH: 256
TYPE: PRT
                                                                                                   -09-077-955-30
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1017 TCLCPPEYTGELCEEKLDFCAQDLNPCQHDSKCILTPRGFKCDCTPGYVGEHCDIDFDDC 1076
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                                                                                                                                                                                                                                                                                                                                 86 RADYVALAIVDGHLQLSYNIGSQPVVIRSTVPVVINRWIRVVAHREQREGSLQVGNEAPV 145
                                                                                                                                                                     -----IELEVRISTASGLLLWOGVEVGEAGO 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELV 208
                                                                                                                                                                                                                                                                                                                                                                                                              209 SGRSPGPNVAVNAKGSVYIGGAPD--VATLIGGRFSSGITGCVKNLVLHSARPGAPPPQP 266
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                                                                                                                                                                                                                                  30 LAFDGRTFVEYLNAVTESELANEIPVEKALQSNHFELSLRTEATQGLVLWS----GKATE 85
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                                                  Query Match
16.7%; Score 261; DB 4; Length 216;
Best Local Similarity 32.8%; Pred. No. 2.4e-16;
Matches 65; Conservative 27; Mismatches 76; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 131; Gaps
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16.2%; Score 253.5; DB 3; Length 1525;
Best Local Similarity 24.8%; Pred. No. 1.6e-14;
Matches 92; Conservative 48; Mismatches 100; Indels 131;
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US-09-191-647-2
US-09-191-647-2
US-09-191-647-2
Sequence 2, Application US/09191647
Fatent No. 6046015
GENERAL INPROMATION:
APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Tessier. Ratja
FILE REPERENCE: B98-013-3
CURRENT APPLICANT: Tessier. Lavigne, Marc
FILE REPERENCE: B98-013-3
CURRENT APPLICANTON: Wodulating Robo: Ligand Interactions
FILE REPERENCE: B98-11-13
FARLIER APPLICATION NUMBER: US/09/191,647
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1998-11-14
FARLIER FILING DATE: 1998-11-14
FARLIER FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                        105 LAFPGHVFSRSLPEVPET---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
US-09-077-955-31
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16.2%; Score 253.5; DB 3; Length 1525;
24.8%; Pred. No. 1.6e-14;
tive 48; Mismatches 100; Indels 131; Gaps 18;
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                      1017 TCLCPPEYTGELCEEKLDFCAQDLNPCQHDSKCILTPKGFKCDCTPGYVGEHCDIDFDDC 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 ------PGQYGA-----YFHDDGFLAFPGHVFSRSLPEVPET-IELEVRISTAS 133
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193 REGRRGSIQVDG--EELVSGRSPGPNVAVNAKGSVYIGGAP---DVATL--TGGRFSSGI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CERQPCQHGATC-MPAGEYE-FQCLCRDGFKGDLCE-----HEENPC------------40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 ---RCQQGSGHGIAESDWHL---EGSGG-------91
                                                                                                                                                                                                                                                                             General information:
General information:
General Corey
APPLICANT: Kid, Thomas
APPLICANT: Kid, Thomas
APPLICANT: Brose, Karly
TILE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR APPLICATION NUMBER: 60/065,544
PRIOR PILING DATE: 1997-11-14
PRIOR PILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                           ; Sequence 2, Application US/09540245A; Patent No. 6270984
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Best Local Similarity 24.84
Matches 92, Conservative
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|301 HGCIRNLYINS 1311
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1301 HGCIRNLYINS 1311
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1525
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// Sequence 2, Application US/09540153
// Patent No. 6270995
// GENERAL INFORMATION:

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957 CISNPCKHGGTCHLKEGEEDGFWCICADGFEGENCEVNVDDCEDNDCENNSTCVDGINNY 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1137 NEPICQCLPGYQGEKCEKLVSVNFINKESYLQIP-----SAKVRPQTN1TLQIATDEDS 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1191 GILLYKG------DKDHIAVELYRGRVRASYDTGSHPASAIYSVETINDGNFHIVELL 1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 ------PGQYGA-----YFHDDGFLAFPGHVFSRSLPEVPET-IBLEVRTSTAS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
16.2%; Score 253.5; DB 3; Length 1525;
Best Local Similarity 24.8%; Pred. No. 1.6e-14;
Matches 92; Conservative 48; Mismatches 100; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ------QGTRCLCLPGFSGP------
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Batent No. 6046015

GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Tesaier-Lavigne, Marc
APPLICANT: Tesaier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3:
CURRENT FILING DATE: 1988-11-13
EARLIER FILING DATE: 1998-11-14
EARLIER PLICATION NUMBER: 60/065,544
EARLIER PLICATION NUMBER: 60/065,544
EARLIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 14

CORMANDE OF SEQ ID NOS: 14
                        APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
APPLICANT: Brose, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFREENCE: B98-031-3.05/09/540,153
CURRENT APPLICATION NUMBER: 09/191,647
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 9
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|1301 HGCIRNLYINS 1311
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Goodman, Corey
Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: human
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SEQ ID NO 2
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Query Match
15.9%; Score 249; DB 3; Length 735;
Best Local Similarity 26.7%; Pred. No. 1.6e-14;
Matches 84; Conservative 48; Mismatches 115; Indels 68; Gaps 17;
                                                                                                  153 ISLGLODGHLVFRYQLGSGEA-RLYSEDPINDGEMHVTALREGRRGSIQVDGE--ELVS 209
                                                                                                                                                                                                                                                       210 GRSPGPNVAVNAKGSVYIGGAP-----DVATLIGGRFSSGIIGCVKNLVLHSARPGAPPP 264
                                                                                                                                                                                                                                                                                                    60 LPGFSG-----FGSGGNDAPGQ 94
; LENGTH: 735

; TYPE: PRT

: ORGANISM: Caenozhabditis elegans

US-09-191-647-9
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Search completed: March 9, 2004, 17:23:33 Job time : 12.1326 sec8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 9, 2004, 17:11:22; Search time 34.5822 Seconds (without alignments) 2320.373 Million cell updates/sec Run on:

Title: Perfect score:

US-10-006-011A-9 1566

1 CEROPCOHGATCMPAGEYEF......OPLDLOHRAQAGANTRPCPS 284 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries 100% Post-processing: Minimum Match 0% Maximum Match 10

A Geneseq 29Jan04:\* 1: qeneseqminosom Database :

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STRAMMIN

		o¥			SUMMARIES		
io .	Sco	Query	eng	DB	ΟΙ	Description	
	1566	100.0	4391	9	AAE34390	34390 Human pe	
8	1559	99.6	4393	4	AAB31889	Amino	
e	1543	98.5	4436	4	ABG23265	Novel	_
4	1030	65.8	195	4	AAB31890	Amino	
Ŋ	357.5	22.8	1931	v	ABU52400		
y	343	21.9	238	4	AAU18145	Novel	_
7	343	21.9	238	4	AAU17011	Human	
ω	343	21.9	238	4	ABB10450	-	_
σ	343	21.9	238	•	AAU19961	Novel	_
10	343	21.9	238	'n	ABJ05772	Novel	_
11	343	21.9	238		ABP67037	Abp67037 Human pol	
12	343	21.9	375	4	AAU07421	Novel	_
13	343	21.9	432	4,	AAU18102	Novel	
74	343	21.9	432	•	AAU16938	Human	
15	343	21.9	432		ABB10233	Human	_
16	343	21.9	432	4	AAU19905	Aau19905 Novel hum	
17	343	21.9	432	Ŋ	ABJ05729		_
18	343	21.9	432		ABP66820	Human	
19	343	21.9	463		ADB64904	Adb64904 Human pro	_
50	343	21.9	671		ABP58231	Human	
21	343	21.9	1009		ADE28105		
22	340.5	21.7	406		ABP41801	Abp41801 Human ova	_
23	338.5	21.6	2053		ADC39154	Adc39154 Novel hum	_
24	80	21.6	2143		ADC39164	Adc39164 Novel hum	_
25	334	21.3	416	N	AAY73993	Aay73993 Human pro	_

Adc39156 Novel hum	Adc39166 Novel hum	Aaw26609 Human agr		_	Abp43859 Human mRN		Aay27141 Human sli	Aaw96706 Protein s	Aay04138 Human sli	Aaw46966 Amino aci	Aay27144 Human sli	Aaw96707 Protein s	Aay04139 Human sli	Ade54473 Human Pro	Aau19782 Human nov	Abp48002 Human pol	Adc10964 Human ext	Abb63614 Drosophil	Abp56528 BM hepara
9	9	On.		23	6	8	1	9	. 00	9	4		6	33	~	2	4	4	8
ADC3915	ADC3916	AAW26609	ABB7229	ADC3916	ABP4385	ABB6194	AAY2714	AAW96706	AAY04138	AAW46966	AAY27144	AAW96707	AAY04139	ADE5447	AAU1978	ABP4800	ADC1096	ABB63614	ABP56528
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1565	1566	492	819	1544	1741	1298	1508	1508	1508	1534	1534	1534	1534	1534	210	210	210	4072	152
21.3	21.3	21.1	21.1	19.8	19.3	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	17.9	17.8
334	334	330	330	310	303	292	292	292	292	292	292	292	292	292	290.5	290.5	290.5	281	279.5
56	27	78	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Human; diagnosis; osteoarthritis; rheumatoid arthritis; perlecan.
                                                                                                                                                          Christgau S, Henriksen DB, Cloos PAC;
                                                                                                                                                                                                                Disclosure; Page 46-67; 106pp; English.
      AAE34390 standard; protein; 4391 AA.
                                                                                                                                             (OSTE-) OSTEOMETER BIO TECH AS.
                                                                                                                  22-MAY-2002; 2002WO-EP005612.
                                                                                                                               23-MAY-2001; 2001GB-00012626.
                                              Human perlecan protein.
                                                                                                                                                                       WPI; 2003-140389/13.
                                                                                       WO200295415-A2.
                                 14-MAY-2003
                                                                                                    28-NOV-2002.
                   AAE34390;
AAE34390
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An assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis comprising detecting an isomerized or optically inverted protein in a sample.

The invention relates to an assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The assay involves measuring (in a biological sample) the amount or presence of an isomerised or optically inverted protein or one or more isomerised or optically inverted fragments from proteins such as perlecan, biglycan, decornin, fibrillin-1 or protocadherin. The assay is useful for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The present sequence is human perlecan protein

Sequence 4391 AA;

Gaps ô Query Match 100.0%; Score 1566; DB 6; Length 4391; Best Local Similarity 100.0%; Pred. No. 8.2e-110; Matches 284; Conservative 0; Mismatches 0; Indels 0;

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4287
                                 4108 CERÓPCOHGATCMPAGEYEFOCLCRDGFKGDLCEHEENPCOLREPCLHGGTCOGTRCLCL 4167
                                                                                                                    PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP 4227
                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                   4288 INDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGR 4347
                                                                              120
                                                                                                                                                            ETIELEVRISTASGLILMQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymucleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the gandjusdide GM2 activator, calgaranlin B or asposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and parkinson's diseases, amyotrophic lateral sclerosis, theumatof polyarthritis and lupus expinematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, perlecan, retinol-binding plasma protein, calgranulin B; vaccine, ganglioside GNZ activator; saposin B; degenerative disease, glial cell; neurological disease, auto-immune disease; multiple sclerosis; toxicity, Alzheimer's disease, Parkinoson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.
                                                                                                                                                                                       4228 BIIELEVRISTASGLLIMQGVEVGEAGGGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
CERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCL
                                                                              PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP
                                                                                                                                                                                                                                             INDGEWHRVTALREGRRGSIOVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charles M, Malcus C, Santoro L, Perron H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting, preventing and treating degenerative, neurological and
                                                                                                                                                                                                                                                                                                                                                      4348 FSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 4391
                                                                                                                                                                                                                                                                                                                             241 FSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 138-152; 209pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31889 standard; protein; 4393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-2000; 2000WO-FR002057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2001 (first entry)
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be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
                                                                                                                                                                                                 4110 CERQPCOHGATCMPAGEYEFQCLCRDGIKGDLCEHEENPCQLREPCLHGGTCQGTRCLCL
                                                                                                                                                                                                                                         PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP
                                                                                                                                                                                                                                                                   4170 PGFSGFRCOQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSKSLPEVP
                                                                                                                                                                                                                                                                                                               121 ETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
                                                                                                                                                                                                                                                                                                                                               4230 ETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
                                                                                                                                                                 1 CERQPCQHGATCMPAGEYEFQCLCRDGFXGDLCEHEENPCQLREPCLHGGTCQGTRCLCL
                                                                                                                                                                                                                                                                                                                                                                                       181 INDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                     99.6%; Score 1559; DB 4; Length 4393; 99.3%; Pred. No. 2.8e-109; ive 1; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4350 PSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 FSSGITGCVKNLVLHSARPGAPPQPLDLQHRAQAGANTRPCPS 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #23256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG23265 standard; protein; 4436
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23-AUG-2000; 2000US-00649167.
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                                                                                                                             Matches 282; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI, 2001-639362/73.
                                                                                                             Local Similarity
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                                                         Sequence 4393 AA;
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4143 CERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEBNPCQLREPCLHGGTCQGTRCLCL 4202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4203 PGFSGPRCQQSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP 4262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP 120
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genes. (1) is useful in gene therapy techniques to restore normal activity of [11] or to treat disease states involving [11]. (11] is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing [11]. (1) and [11] are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymouteotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CERQPCQHGATCMPAGEYEFQCLCRDGPKGDLCEHEENPCQLREPCLHGGTCQGTRCLCL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 98.5%; Score 1543; DB 4; Length 4436; Local Similarity 96.2%; Pred. No. 4.7e-108; nes 282; Conservative 0; Mismatches 1; Indels 10,
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The present sequence represents a human polypeptide, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymuleotide sequence belonging to the perfecan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GW2 activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a capturelative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and parkinson's diseases, amyotophic lateral sclerosis, rheumatoid polyarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 DAPGOYGAYFHDDGFLAFPGHVPSRSLPEVPETIELEVRISTASGLLLWQGVEVGEAGQG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KDFISLGLODGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                          Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQPLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPQPLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPETIBLEVRTSTASGLLLWQGVEVGEAGOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 KDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.8%; Score 1030; DB 4; Length 195; 100.0%; Pred. No. 1.5e-70; tive 0; Mismatches 0; Indels
                                                                                                                                                         Claim 1; Page 152-153; 209pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU52400 standard; protein; 1931 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human GPCR related protein NOV40a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2001; 2001US-0274281P. 08-MAR-2001; 2001US-0274322P. 09-MAR-2001; 2001US-0274849P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2002; 2002WO-US007355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 QHRAQAGANTRPCPS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 OHRAQAGANTRPCPS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAR-2003 (first entry)
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                 WPI; 2001-159475/16.
N-PSDB; AAF54728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 195 AA;
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Claim 1; Page 223; 413pp; English.
       13-WAR-2001; 2001US-0275579F.
14-WAR-2001; 2001US-0275579F.
14-WAR-2001; 2001US-0275601P.
14-WAR-2001; 2001US-0276994P.
20-WAR-2001; 2001US-0277339F.
20-WAR-2001; 2001US-0277339F.
21-WAR-2001; 2001US-0277339F.
22-WAR-2001; 2001US-0277339F.
23-WAR-2001; 2001US-0277339F.
23-WAR-2001; 2001US-0278999F.
27-WAR-2001; 2001US-0278999F.
27-WAR-2001; 2001US-0278999F.
27-WAR-2001; 2001US-0278999F.
27-WAR-2001; 2001US-0280802F.
30-WAY-2001; 2001US-0280802F.
02-WAY-2001; 2001US-0280802F.
02-WAY-2001; 2001US-0298086F.
07-JUN-2001; 2001US-0296856F.
05-JUL-2001; 2001US-0296856F.
05-JUL-2001; 2001US-0398330F.
05-JUL-2001; 2001US-0398330F.
05-JUL-2001; 2001US-0398330F.
05-JUL-2001; 2001US-0398330F.
05-JUL-2001; 2001US-0398330F.
05-JUL-2001; 2001US-0398330F.
                                                                                                                                                                                                                                                                      16-AUG-2001; 2001US-0312916P.
17-AUG-2001; 2001US-0313182P.
20-AUG-2001; 2001US-0313626P.
                                                                                                                                                                                                                                                                                                   21-AUG-2001; 2001US-0314018P.
27-AUG-2001; 2001US-0315227P.
10-SEP-2001; 2001US-0318403P.
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                                                                                                                                                                                                                                                                       16-AUG-2001;
17-AUG-2001;
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The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOVI-NOV4), variants of these proteins, and the polynucleotide sequences encoding them. The NOVI proteins of the invention are G-protein coupled receptor (GPCR) related proteins. The sequences of the invention are useful in the manufacture of a medicament for reating a syndrome related to a human disease associated with the polypeptides e.g. cancer. ABUS2111-ABUS2408 represent the human NOVX proteins of the invention
Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
Guo X, Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ;
Pena CEA, Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;
Pochart PR, Fernandes ER, Shimkets RA, Rastelli L, Spaderna SK;
Larochelle WJ, Zhong M, Khramtsov NV, Voss EZ, Herrmann JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOVX polypeptides and polynucleotides, useful for treating a syndrome related to a human disease associated with the NOVX polypeptide e.g., cancer.
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Score 357.5; DB 6; Length 1931; Pred. No. 3.1e-18;
                           35.4%;
                             Query Match
Best Local Similarity
Sequence 1931 AA;
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1498 OCECPLGREGIFCOTAS------GODGSGPFLADFNGFSHLELRGLHTFAR 1542
8
                                    1439 CLPNPCHGGAPCQNLEAGRFHCQCPPGRVGPTCADEKSPCQ-PNPCHGAAPCRVLPEGGA 1497
                                                                                                                           1543 DLGE-KMALEVVFLARGPSGLLLYNGOKTD--GKG-DFVSLALRDRRLEFRYDLGKGAAV 1598
                                                                                                                                                                   56 RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                            115 SLPEVPETIELEVRISTASGLILMQGVEVGEAGQGKDPISLGLQDGHLVFRYQLGSGEAR 174
                                                                                                                                                        175 LVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVA 234
                                                                                                                                                                                                                                                                                                                                                                      Human; uterine motility-association disorder; uterus; pregnancy; labour;
                       1 CERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQ----GT
 91; Conservative 29; Mismatches 110; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                Novel human uterine motility-association polypeptide #52.
                                                                                                                                                                                                                                                                                 AAU18145 standard; protein; 238 AA.
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                                                                                                                                                                                                    235 TLT-GGRFSSGITGCVK 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180628P.
2000US-0184664P.
2000US-018636P.
2000US-0190076P.
2000US-0190133P.
2000US-020515P.
2000US-020515P.
2000US-0214886P.
2000US-0215135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0216880P.
200US-0217487P.
200UUS-0217496P.
200UUS-0218290P.
2000US-0220963P.
                                                                                                                                                                                                                                                                                                                                                                                    menstrual cycle; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                              WO200155201-A1.
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
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11-JUL-2000;
11-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
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PR 14-AUG-2000, 2000UG-0225759P.
PR 22-AUG-2000, 2000UG-0222686PP.
PR 22-AUG-2000, 2000UG-0222686PP.
PR 22-AUG-2000, 2000UG-0227182P.
PR 23-AUG-2000, 2000UG-0227184P.
PR 01-SEP-2000, 2000UG-0227184P.
PR 06-SEP-2000, 2000UG-0227184P.
PR 08-SEP-2000, 2000UG-0227184P.
PR 08-SEP-2000, 2000UG-023739P.
PR 14-SEP-2000, 2000UG-023739P.
PR 27-SEP-2000, 2000UG-023739P.
PR 20-CCT-2000, 2000UG-023739P.
PR 20-CCT-2000, 2000UG-023709P.
PR 20-CCT-2000
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The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and amourt, and menstrual disorders. The polymucleotide sequences of the invention are also useful in gene therapy. AAD18094-AAD18152 represent novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ENAAHPC-VRAPCAHGGSCRPRKEGYDCDCPLGFEGLHCQKAIIEAI------ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 EHEENPCOLREPCLHGGTC----OGTRCLCLPFGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query,Match
21.9%; Score 343; DB 4; Length 238;
Best Local Similarity 33.5%; Pred. No. 3.6e-18;
Matches 86; Conservative 34; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 121; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Barash SC, Ruben SM;
           08-NOV-2000; 2000US-02456L3P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
18-DEC-2000; 2000US-025198P.
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N-PSDB; AAS28987.
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
31-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                            05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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20-007-2000
20-007-2000
20-007-2000
20-007-2000
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10-007-2000
10-007-2000
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08-NOV-2000;
08-NOV-2000;
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29-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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27-SEP-2000;
29-SEP-2000;
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14-SEP-2000;
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                                                                                                                                                                                                                                                                               25-SEP-2000
Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; eartibacterial; virucide; fungloide, opthalmalogical; vulnerary; secreted protein; rheumatoid atthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                  146 AGOGKOFISLGLODGHLVFRYQLGSGBARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                           206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                                     166 GARTGKSPGWMRQLNINGALYVGGMKEIALHTWRQYWRGLVGCISHFTLST-----DY
                                                                                                                                                                                                 Human novel secreted protein, SEQ ID 252.
                                                                                                                                            AAU17011 standard; protein; 238 AA.
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24-FEB-2000; 2000US-0184664P.
16-MAR-2000; 2000US-01850F.
17-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-01913P.
19-MAY-2000; 2000US-020515P.
07-UN-2000; 2000US-0214886F.
30-UNM-2000; 2000US-0214886F.
                                                                             266 PLDLQHRAQAGANTRPC 282
                                                                                              219 HISLVEDAVDGKNINTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -JUL-2000; 2000US-0216880P.
-JUL-2000; 2000US-0217487P.
-JUL-2000; 2000US-0217496P.
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26-JUL-2000; 2000US-0220963P.
26-JUL-2000; 2000US-0220964P.
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                                                                                                                                                                              07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                            WO200155441-A2.
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2000US-0236367P.
2000US-0236368P.
2000US-0236369P.
2000US-0232401P
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Rosen CA, Barash SC, Ruben SM;
                                17.NOV-2000; 2000US-02492109: 17.NOV-2000; 2000US-02492109: 17.NOV-2000; 2000US-02492109: 17.NOV-2000; 2000US-02492119: 17.NOV-2000; 2000US-0249213P: 17.NOV-2000; 2000US-0249214P: 17.NOV-2000; 2000US-0249218P: 17.NOV-2000; 2000US-024924P: 17.NOV-2000; 2000US-024929P: 17.NOV-2000; 2000US-024929P: 01.DEC-2000; 2000US-025199P: 05-DEC-2000; 2000US-025199P: 06-DEC-2000; 2000US-025198P: 06-DEC-2000; 2000US-0251869P: 08-DEC-2000; 2000US-0251869P: 08-DEC-2000; 2000US-0251869P: 08-DEC-2000; 2000US-0251869P: 08-DEC-2000; 2000US-0251869P: 08-DEC-2000; 2000US-0251969P: 08-DEC-2000; 2000US-
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N-PSDB; AAS26916.
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Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 11; SEQ ID NO 252; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a late also be used in alleviating symptoms associated with the disorders and in diagnostic indiagnostic symptoms associated with the disorders and in diagnostic immunosespape e.g. radioimmunoassays or enzyme linked immunoserbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cerebral schaemia, angiogenesis, necroplasms of the breast or liver, cardiovascular disorders e.g. corneal infection, nervous system disorders e.g. Altheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, can also be used to aid wound healing and epithelial cell proliferation, cransplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotrais. The polypeptides can also be used cornears at foot additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, miterals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The

21.9%; Score 343; DB 4; Length 238; 33.5%; Pred. No. 3.6e-18; Query Match Best Local Similarity

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                                                                                                                                                            90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
                                                                          146 AGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                    206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                 34 EHEENPCQLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
 40; Gaps
                                                                                                                                                                                                                                                                                                                                                    Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
 97; Indels
 86; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                     ABB10450 standard; protein; 238 AA.
                                                                                                                                                                                                              219 HISLVEDAVDGKNINTC 235
                                                                                                                                                                                          266 PLDLQHRAQAGANTRPC 282
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2000US-0220963P.
2000US-0220964P.
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2000US-0198123P.
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2000US-0214B86P.
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2000US-0186350P.
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                                                                                                                                                                                                                                                                                                                                  Human cDNA SEQ ID NO: 758.
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116-MAR-2000)
117-MAR-2000)
119-MAY-2000)
07-UUN-2000)
30-UUN-2000)
30-UUN-2000)
07-UUL-2000)
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14-AUG-2000;
14-AUG-2000;
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111-JUL-2000;
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26-JUL-2000;
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14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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  Matches
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ABB10450
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18-ANG-2000; 2000US-0226279P; 22-ANG-2000; 2000US-0226681P; 22-ANG-2000; 2000US-0226681P; 22-ANG-2000; 2000US-0228945P; 01-SEP-2000; 2000US-0228945P; 01-SEP-2000; 2000US-0229945P; 01-SEP-2000; 2000US-0229945P; 01-SEP-2000; 2000US-0229945P; 02-SEP-2000; 2000US-0229945P; 03-SEP-2000; 2000US-0229945P; 04-SEP-2000; 2000US-0229945P; 06-SEP-2000; 2000US-0229945P; 06-SEP-2000; 2000US-0229945P; 06-SEP-2000; 2000US-0229945P; 06-SEP-2000; 2000US-0229945P; 06-SEP-2000; 2000US-023949P; 06-SEP-2000; 2000US-0231441P; 06-SEP-2000; 2000US-0231444P; 06-SEP-2000; 2000US-0231494P; 06-SEP-2000; 2000US-02314994P; 06-SEP-2000; 2000US-0231494P; 06-SEP-2000; 2000US-0231494P; 06-SEP
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57 BIPQFIGRSYLTYDNPDILKRVSG---SRS-----NVFMRFKTTAKDGLLLMRG--DSP 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 EHEENPCOLREPCLHGGIC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.
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21.9%; Score 343; DB 4; Length 238;
Best Local Similarity 33.5%; Pred. No. 3.6e-18;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 758; 859pp + Sequence Listing; English
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08-NOV-2000; 2000US-0246609F.
08-NOV-2000; 2000US-0246613P.
08-NOV-2000; 2000US-0246613F.
17-NOV-2000; 2000US-0249207F.
17-NOV-2000; 2000US-0249207F.
17-NOV-2000; 2000US-0249208F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249213F.
17-NOV-2000; 2000US-0249214F.
17-NOV-2000; 2000US-0249214F.
17-NOV-2000; 2000US-0249214F.
17-NOV-2000; 2000US-0249218F.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-024926FF.
17-NOV-2000; 2000US-025198F.
18-DEC-2000; 2000US-025198F.
18-DEC-2000; 2000US-025186FF.
18-DEC-2000; 2000US-025186FF.
18-DEC-2000; 2000US-025186FF.
18-DEC-2000; 2000US-025186FF.
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N-PSDB; ABA06672.
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06-SEP-2000;

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06-SEP-2000;

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14-SEP-2000;

15-SEP-2000;

16-SEP-2000;

17-SEP-2000;

17-SEP-2000;

18-SEP-2000;

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29-58P-2000
29-58P-2000
29-58P-2000
20-0CT-2000
20-0CT
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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     206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; calcium-binding protein; calcium flux; neurological disease;
immune dysfunction; digestive disorder; neoplastic disease;
blood disorder; infectious disease; gene therapy; immunosuppressive;
antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human calcium-binding protein #70.
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24-PEB-2000; 2000US-01864664P.

25-PAR-2000; 2000US-0186450P.

10-PAR-2000; 2000US-0186450P.

11-PAR-2000; 2000US-0186450P.

11-PAR-2000; 2000US-0190016P.

11-JUN-2000; 2000US-0190016P.

26-JUN-2000; 2000US-0214886P.

11-JUL-2000; 2000US-0214886P.

11-JUL-2000; 2000US-0214886P.

11-JUL-2000; 2000US-0214886P.

11-JUL-2000; 2000US-021689P.

11-JUL-2000; 2000US-021689P.

11-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0218290P.

26-JUL-2000; 2000US-0218290P.

14-AUG-2000; 2000US-022566P.

14-AUG-2000; 2000US-022576P.

14-AUG-2000; 2000US-0225779P.

22-AUG-2000; 2000US-0225779P.

22-AUG-2000; 2000US-0225779P.

22-AUG-2000; 2000US-0225779P.

22-AUG-2000; 2000US-0225779P.
                                                                                                                     266 PLDLOHRAQAGANTRPC 282
                                                                                                                                                                  219 HISLVEDAVDGKNINTC 235
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2000US-0230437P
2000US-0231243P
2000US-0231244P
2000US-0231244P
2000US-02314144P
2000US-02314144P
2000US-0232080P
2000US-0232080P
2000US-0232080P
2000US-0232399P
2000US-0232399P
2000US-0232399P
2000US-0232399P
2000US-0232399P
                                                                                                                                                                                                                                                                                                                                                           20000S-0235484P

20000S-0235834P

20000S-023636P

20000S-02363993P

20000S-024096P

20000S-024096P

20000S-024186P

20000S-0246474P

20000S-0246477P

20000S-0246477P

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20000S-0246477P
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2000US-0233065P.
2000US-0234223P.
2000US-0234274P.
2000US-0234997P.
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2000US-0246528P.
2000US-0246532P.
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Page 10

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206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPQ 265
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01-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel human calciumbidding proteins, and cDNA (AAA31577-AAA31654) and genomic sequences of encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19952-AAU19969 represent the novel human calcium-binding the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
                     17-NOV-2000; 2000US-0249216F.
17-NOV-2000; 2000US-0249217F.
17-NOV-2000; 2000US-0249248F.
17-NOV-2000; 2000US-0249244F.
17-NOV-2000; 2000US-0249264F.
17-NOV-2000; 2000US-0249264F.
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08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0255678P.
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05-DEC-2000; 2000US-025198BP
05-DEC-2000; 2000US-0256719P
06-DEC-2000; 2000US-0251479P.
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08-DEC-2000; 2000US-0251868P-
08-DEC-2000; 2000US-0251869P-
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N-PSDB; AAS31646.
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11 ENAAHPC-VRAPCAHGGSCRPRKEGYDCDCPLGFEGLHCOKAIIEAI------

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Immunostimulant; antirheumatic; antiarthritic; neuroprotective; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabeticy; noctropic; immunosuppressive; antidiabetic; antidiatherory; noctropic; cytostatic; nephrotropic; antipart; thrombolytic; antiatherosclerotic; ortostatic; nephrotropic; antiparkinsonian; gynecological; virucide; antibacterial; antiarrhythmic; fungicide; HGRAGS; HMRABNO1; immunodeficiency; autoimmune; disorder; allergic reaction; cardiovascular; inflammatory condition; graft-versus-host disease; reproductive system; blod-related disorder; hyperproliferative; endocrine; neurological; respiratory; renal; infectious disease; gastrointestinal; gene therapy; neuropal growth; neuropal disorder; neuro-degenerative condition;
166 GARTGKSPGWARQLNINGALYVGGMKEIALHTURQYWRGLVGCISHFTLST-----DY 218
                                                                                                                             ABJ05772 standard; protein; 238 AA
                                                                                                                                                                                                        Novel human protein SEQ ID No 121.
                                                             219 HISLVEDAVDGKNINTC 235
                                    266 PLDLOHRAQAGANTRPC 282
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2000US-0218290P.
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11-UUL-2000;
14-UUL-2000;
26-UUL-2000;
26-UUL-2000;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated polypeptide comprising a sequence at least 90% identical to a full length protein sequence selected from 55 sequences given in the specification sequence selected from 55 sequences given in the specification, or the encoding sequence of 163, 74 or 140 amino acids fully defined in the specification, or the encoding sequence or HTMSMO1. The protein and its encoding nucleic acid are useful for the appropriate and its encoding nucleic acid are useful for diagnosing a pathological condition in a subject and for preventing, treating or ameliorating a medical condition. The protein its encoding nucleic acid and an isolated antibody that can bind to the protein are useful in treating, preventing, diagnosing and/or prognosing immunodeficiencies, autoinmune disorders, allergic reactions and conditions, inflammatory conditions, graft-versus-host disease, blood-related disorders, hyperproliferative disorders, neurological disorders, endocrine disorders, reproductive system disorders, and/or diagnose neuronal disorders. The protein of the invention is useful to stimulate neuronal gisorders and/or diagnose neuronal damage which occurs in certain characteristics such as body height, weight, hair color, and to increase or decrase storage capabilities, fat content, lipid, protein, or decrase storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The mucleic acid of the invention can be used in gene therapy. This sequence represents a novel human protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 EHEENPCQLREPCLHGGTC---QGTRCLCLPGPSGPRCQQGSGHGIAESDWHLEGSGGN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 287-288; 335pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC;
                                                                                                             02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-023935P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-0241869P.
01-NOV-2000; 2000US-0244617P.
                                                                             02-OCT-2000; 2000US-0237038P.
                                                                                                                                                                                                                                  17-NOV-2000; 2000US-0249299P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
                                                                                                                                                                                                                                                                                                08-DEC-2000; 2000US-0251869P.
                                                         02-OCT-2000; 2000US-0237037P
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Best Local Similarity 33...
Thes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-665432/71
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                                                                                                                                                                                                                                                                                                                                     ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
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166 GARTGKSPGMRQLNINGALYVGGMKEIALHTNRQYMRGLVGCISHFTLST-----DY 218
                                  206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; valnetary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antialaregic; antidiabectic; antilloer; anticonvallsant; antimagal; antiparasitic; cardiant; immune discorder; cardiovascular discorder; neurological discase; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                            ABP67037 standard; protein; 238 AA.
                                                                                                                                                                                                                              Human polypeptide SEQ ID NO 758.
                                                                             266 PLDLOHRAQAGANTRPC 282
                                                                                                    219 HISLVEDAVDGKNINTC 235
                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001US-00764853
                                                                                                                                                                                                        09-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   US2002090672-A1.
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26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                        146 AGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
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The invention relates to novel genes (ABV83682-ABV84101) and proteins (ABP66710-ABP67129) useful for preventing, treating or ameliorating isolated aconditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast gastrointestinal tract, liver, lung, or urogenital; (b) immune hasenia, autoimmune thyroiditis, diabetes mellitus, Crobn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 EIPOFIGRSYLTYDNPDILKRVSG---SRS-----NVFMRFKTTAKDGLLLWRG--DSP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 EHEENPCQLREPCLHGGTC---QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.9%; Score 343; DB 5; Length 238; larity 33.5%; Pred. No. 3.6e-18; Conservative 34; Mismatches 97; Indels 40; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 758; 369pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                Barash SC;
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                                                                                              02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
20-OCT-2000; 2000US-0240960P.
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17-NOV-2000; 2000US-0249299P.
08-DEC-2000; 2000US-0251856P.
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20-OCT-2000; 2000US-0241809P.
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                                                                             2000US-0237039P
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les 86; Conserva
                                                                                                                                                                                                                                                                                                                  (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                       (BARA/) BARASH S C.
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                                    02-OCT-2000;
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C. The invention relates to novel isolated polynuclectides (I) encoding extracellular matrix (ECM) polypeptides. (I) and a polypeptide encoded by (I) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the polypeptides can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays [ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. rheumatoid arthritis hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, virtuses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound be aling and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell collypeptides can also be used as a food additive or preservative to increase storage capabilities. The presents the amino acid sequence of novel human extracellular matrix
                                                                                                                                                                                                                                                                                                                           antiproliferative; cardiant; vasotropic; cerebroprotective; nootropic; neucoprotective; antibacterial; virucide; fungicide; ophthalmological; extracellular matrix; ECM; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiat; cerebral ischaemia; infection; nervous system disorder; Albhelmer's disease; ocular disorder; sunburn; wound healing; food additive.
                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding extracellular matrix polypeptides, for diagnosing, treating, preventing or ameliorating human disorders ar disease, such as, autoimmune, hyperproliferative or cardiovascular
                                                                                                                                                                                                                                                               Novel human extracellular matrix (ECM) protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fiscella M, Shi Y, Ebner R, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 297-298; 308pp; English.
                                                                                                                             AAU07421 standard, protein; 375 AA.
219 HISLVEDAVDGKNINTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2001; 2001WO-US011643.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                 18-DEC-2001 (first entry)
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                                                                                                                                                                        AAU07421;
                                                                               RESULT 1.
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21.9%; Score 343; DB 4; Length 375;

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90 DAP----GQYGAYFHDDGFLAPPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGE 145
                                                                                                                                                                  146 AGGGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                                              243 MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGGSGKITVDDY 302
                                                                                                                                                                                                                                                                                                      206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
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                                                            34 RHEENPCOLREPCINGGTC----QTRCLCLPGRSGPRCQQGSGHGIAESDWHLEGSGGN 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; uterine motility-association disorder; uterus; pregnancy; labour; menstrual cycle; gene therapy.
Best Local Similarity 33.5%; Pred. No. 6.1e-18;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human uterine motility-association polypeptide #9.
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24-FEB-2000; 2000US-0180628P.
16-MAR-2000; 2000US-01896464P.
16-MAR-2000; 2000US-0189874P.
19-MAY-2000; 2000US-0189874P.
19-MAY-2000; 2000US-0198123F.
19-MAY-2000; 2000US-0208467P.
28-JUN-2000; 2000US-0218135P.
07-JUL-2000; 2000US-0218135P.
07-JUL-2000; 2000US-0218488P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0221829P.
14-AUG-2000; 2000US-0228519P.
14-AUG-2000; 2000US-0228514P.
                                                                                                                                                                                                                                                                                                                                                                                  266 PLDLOHRAQAGANTRPC 282
                                                                                                                                                                                                                                                                                                                                                                                                                356 HISLVEDAVDGKNINTC 372
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14-AUG-2000; 2000US-0225270P.
14-AUG-2000; 2000US-0225447P.
14-AUG-2000; 2000US-0225787P.
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PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0225759P.
PR 22-AUG-2000; 2000US-022668P.
PR 22-AUG-2000; 2000US-022668P.
PR 22-AUG-2000; 2000US-022668P.
PR 23-AUG-2000; 2000US-022789P.
PR 23-AUG-2000; 2000US-0229445P.
PR 01-SEP-2000; 2000US-0229445P.
PR 02-SEP-2000; 2000US-0229445P.
PR 02-SEP-2000; 2000US-0229445P.
PR 03-SEP-2000; 2000US-0229445P.
PR 03-SEP-2000; 2000US-0229445P.
PR 03-SEP-2000; 2000US-0229445P.
PR 03-SEP-2000; 2000US-0231443P.
PR 03-SEP-2000; 2000US-0231443P.
PR 03-SEP-2000; 2000US-0231443P.
PR 03-SEP-2000; 2000US-0231443P.
PR 14-SEP-2000; 2000US-0231443P.
PR 25-SEP-2000; 2000US-023143P.
PR 25-SEP-2000; 200
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146 AGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                 360 GARTGKSPGMARQLNINGALYVGGMKEIALHTNRQYMRGLVGCISHFTLST-----DY 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; alfacimer; angiogenesis; nervous system disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
251 EIPQFIGRSYLTYDNPDILKRVSG---SRS----NVFMRFKTTAKDGLLLWRG--DSP 299
                                                                              300 MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSGKITVDDY 359
                                                                                                                        206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                        AAU16938 standard; protein; 432 AA.
                                                                                                                                                                                                         266 PLDLQHRAQAGANTRPC 282
                                                                                                                                                                                                                                                  413 HISLVEDÁVDGKNINTC 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-2001 (first entry)
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                             a
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                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human uterine motility association polypeptides, and cDNA (MAS28936-AAS28994) and motility association polypeptides, and cDNA (MAS28996-AAS28994) and enough the sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polymucleotide sequences of the invention are also useful in gene therapy, AAU18094-AAU18152 represent novel human uterine motility-association polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.9%; Score 343; DB 4; Length 432; Best Local Similarity 33.5%; Pred. No. 7.1e-18; Matches 86; Conservative 34; Mismatches 97; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 78; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-2001; 2001US-0259678P.
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                                                                              24920BP
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01-DEC-2000;
05-DEC-2000;
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2000US-0225759P

14-AUG-2000;

90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145

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34 EHEENPCOLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89

97; Indels 40; Gaps

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18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-02216868P.
22-AUG-2000; 2000US-02216868P.
23-AUG-2000; 2000US-02216868P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229344P.
06-SEP-2000; 2000US-0239344P.
06-SEP-2000; 2000US-0231243P.
06-SEP-2000; 2000US-0231243P.
06-SEP-2000; 2000US-0231243P.
06-SEP-2000; 2000US-0231398P.
14-SEP-2000; 2000US-0231398P.
14-SEP-2000; 2000US-0233968P.
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29-SEP-2000; 2000US-0236368P

29-SEP-2000; 2000US-0236368P

29-SEP-2000; 2000US-0236369P

22-OCT-2000; 2000US-0236370P

02-OCT-2000; 2000US-0237038P

02-OCT-2000; 2000US-0237038P

02-OCT-2000; 2000US-0237038P

13-OCT-2000; 2000US-0237038P

13-OCT-2000; 2000US-0237038P

20-OCT-2000; 2000US-0237038P

20-OCT-2000; 2000US-0237038P

20-OCT-2000; 2000US-024188SP

20-OCT-2000; 2000US-024188P

20-OCT-2000; 2000US-024188P

20-OCT-2000; 2000US-024180P

20-OCT-2000; 2000US-024647P

08-NOV-2000; 2000US-024647P

08-NOV-2000; 2000US-024647P

08-NOV-2000; 2000US-024647P

08-NOV-2000; 2000US-024652P

08-NOV-2000; 2000US-024652P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000; 2000US-0234274P.
25-SEP-2000; 2000US-0234999P.
25-SEP-2000; 2000US-0234998P.
27-SEP-2000; 2000US-0235484P.
27-SEP-2000; 2000US-0235434P.
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Rosen CA, Barash SC, Ruben SM;
      17.NOV-2000; 2000US-0249207F.
17.NOV-2000; 2000US-0249207F.
17.NOV-2000; 2000US-0249207F.
17.NOV-2000; 2000US-0249207F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249217F.
17.NOV-2000; 2000US-0249218F.
17.NOV-2000; 2000US-024924F.
17.NOV-2000; 2000US-024924F.
17.NOV-2000; 2000US-024924F.
17.NOV-2000; 2000US-024926F.
17.NOV-2000; 2000US-025198F.
18.DEC-2000; 2000US-025186F.
19.DEC-2000; 2000US-025186F.
19.DEC-2000; 2000US-025186F.
10.DEC-2000; 2000US-025186F.
10.DEC-2000; 2000US-025186F.
11.DEC-2000; 2000US-025186F.
11.DEC-2000; 2000US-025186P.
                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476222/51.
N-PSDB; AAS26843.
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Novel polypeptides and polynucleotides useful as diagnostic reagents the diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, hemophilia.

Claim 11; SEQ ID NO 179; 601pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or amaliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ILISA). Disorders which are diagnosed or treated include autoimmune classes e.g. rheumatcid arthitis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. crebrish is stocked by netrous system disorders e.g. Alzheimer's disease, infections caused by becteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, for supporting cell culture of primary tissues, to resentate tissues and in chemotrasis. The polypeptides can also be used diditive or preservative to increase or decrease storage as food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, ocfactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The

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14-AUG-2000; 2000UG-022575 P.

14-AUG-2000; 2000UG-022575 P.

14-AUG-2000; 2000UG-022575 P.

14-AUG-2000; 2000UG-022575 P.

12-AUG-2000; 2000UG-022575 P.

12-AUG-2000; 2000UG-022718 P.

22-AUG-2000; 2000UG-022718 P.

22-AUG-2000; 2000UG-022718 P.

23-AUG-2000; 2000UG-022718 P.

24-SEP-2000; 2000UG-02374 P.

25-SEP-2000; 2000UG-02374 P.

26-SEP-2000; 2000UG-02374 P.

27-SEP-2000; 2000UG-02374 P.

28-SEP-2000; 2000UG-02370 P.

28-SEP-2000; 2000UG
      205 ENAAHPC-VRAPCAHGGSCRPRKEGYDCDCPLGFEGLHCQKAIIEAI------250
                                                                                                                     90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
                                                                                                                                                           146 AGQGKDFISLGLQDGHLVFRYQLGSGBARLVSEDPINDGBWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                 206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQ 265
                                              34 EHEENPCOLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89
    Best Local Similarity 33.5%; Pred. No. 7.1e-18;
Matches 86; Conservative 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
                                                                                                                                                                                                                                                                                                                                                                          ABB10233 standard; protein; 432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04 FEB-2000; 2000US-0180628P.
02-MAR-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0189374P.
16-MAR-2000; 2000US-0189374P.
18-APR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-021813P.
28-JUN-2000; 2000US-021813P.
07-JUL-2000; 2000US-021813P.
07-JUL-2000; 2000US-021819P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
11-JUL-2000; 2000US-02189P.
14-JUL-2000; 2000US-02189P.
14-MUS-2000; 2000US-02189P.
14-AUG-2000; 2000US-02189P.
14-AUG-2000; 2000US-022899P.
14-AUG-2000; 2000US-022899P.
14-AUG-2000; 2000US-022899P.
14-AUG-2000; 2000US-022899P.
14-AUG-2000; 2000US-022899P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA SEQ ID NO: 541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200154474-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                    ABB10233;
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us-10-006-011a-9.rag

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The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastroincestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.9%; Score 343; DB 4; Length 432;
33.5%; Pred. No. 7.1e-18;
ive 34; Mismatches 97; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 541; 859pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC, Ruben SM;
        08-NOV-2000; 2000US-0246610P

08-NOV-2000; 2000US-0246610P

08-NOV-2000; 2000US-0246611P

08-NOV-2000; 2000US-0246611P

17-NOV-2000; 2000US-024920P

17-NOV-2000; 2000US-024920P

17-NOV-2000; 2000US-0249210P

17-NOV-2000; 2000US-0249210P

17-NOV-2000; 2000US-0249211P

17-NOV-2000; 2000US-0249212P

17-NOV-2000; 2000US-0249213P

17-NOV-2000; 2000US-0249213P

17-NOV-2000; 2000US-0249214P

17-NOV-2000; 2000US-0249215P
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06-DEC-2000; 2000US-0251479P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251989P.

11-DEC-2000; 2000US-025199P.

05-JAN-2001; 2001US-025997P.
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17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
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17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
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L7-NOV-2000; 2000US-0249299P.
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01-DEC-2000; 2000US-0250391P.
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                                                                                                                                                                                                                                                                                                                                                         ; 2000US-0249300P.
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Best Local Similarity 33.54
Matches 86; Conservative
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N-PSDB; ABA06455.
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17-NOV-2000;
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251 EIPOPIGRSYLTYDNPDILKRVSG---SRS-----NVFMRFKTTAKDGLLLWRG--DSP 299

146 AGQCKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205

90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLMQGVEVGE 145

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34 EHBENPCOLREPCINGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGN 89

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206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                                                    360 GARTGKSPGMORQLNINGALYVGGMKEIALHTURQYMRGLVGCISHFTLST-----DY 412
300. MRPNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSGKITVDDY 359
                                                                                                                                                                                                                                              9, 2004, 17:19:03
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Job time: 35.5822 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:11:52 ; Search time 17.0517 Seconds (without alignments) 2152.832 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-006-011A-3 3825 1 EIKITFRPDSADGMLLYNGQ.......QPLDLQHRAQAGANTRPCPS 705

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Query Match Length	4	3707	1959	1955	1328	3375	3313	1715	1712	1477	1530	1514	3301	1529	3312	1541	1363	2144	5147	3579	2923	1578	2920	3110	1310	3084	3075	3097	3106	1504	2471	4705	3672
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	Result No.	1	7	m	4	'n	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20	30	31	32	33

Q9nyq6 homo sapien	Q9qw30 rattus norv									
CLR1_HUMAN.	NTC2 RAT	NTC3_HUMAN	NTC2 MOUSE	NTC4 HUMAN	NTC3_RAT	NTC3 MOUSE	CLR1 MOUSE	CTA4 HUMAN	CTA2 HUMAN	JAG1_RAT
Н.	4 ~	Н	Н	Н	Н	<b>,</b>	Н	Н	Н	Н
3014	2471	2321	2470	2003	2319	2318	3034	1308	1331	1219
80 c	# m	8.3	8.5	8.7	8.1	8.1	8.1	8.1	7.9	0.
325	319	316	314.5	312	311.5	311	311	310.5	303.5	302.5
34	0 9 9	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  PORTH HUMAN STANDARD; PRT; 4391 AA.  TO PORTH HUMAN STANDARD; PRT; 4391 AA.  PORTH HUMAN STANDARD; PRT; 4391 AA.  TO PORTH HUMAN STANDARD; PRT; 4391 AA.  OI -OCT-1996 (Rel. 34, Created)  TO PERS-2003 (Rel. 42, Last sequence update)  DT 10-0CT-2003 (Rel. 42, Last sandcation update)  B Assement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).  B HSPG2.  HUMC sapiens (Human n).  SEQUENCE FROM N.A.  RA MEDINE-S1212994; PubMed=1730768;  RA Allunki P., Trygyason K.;  RA MEDINE-S1212994; PubMed=1730768;  RA Allunki P., Trygyason K.;  RA Allunki P., Trygyason K.;  RA MEDINE-S1215994; PubMed=1730768;  RY I)  CO COLL Biol. 116:559-571(1992).  RY SEQUENCE FROM N.A.  RY Decules, and epidermal growth factor.";  AN GOURNE FROM N.A.  RY SEQUENCE FROM N.A.  RY Decules, and Skin;  RY SEQUENCE FROM N.A.  RY SEQUENCE RY SECUENCE PROPERTY SECOND N.A.  RY SEQUENCE RY SECUENCE PROPERTY SECOND N.A.  RY SEQUENCE RY SECUENCE RY SECUENCE PROPERTY SECOND N.A.  RY SEQUENCE RY SECUENCE RY SECUEN	MEDLINE=20553141; PubMed=11101850; Nicola S., Davoine C18., Topaloglu H., Cattolico L., Barral D., Nicola S., Davoine C18., Topaloglu H., Cattolico L., Matte P.S., Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J., Hentrati P., Fontaine B.; Hentrati P., Fontaine B.; Perlecan, the major proteoglycan of basement membranes, is altered in patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia)."; Nat. Genet. 26:480-483(2000).  [4] SEQUENCE OF 1016-1470 FROM N.A. TISSUES-COlon, MEDLINE-91365376; PubMed=1679749; Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W., Yi H.F., IOZZO R.V.; Yi H.F., IOZZO R.V.; Yi H.F., IOZZO R.V.; Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular expression, and mapping of the gene (HSPG2) to the short arm of human chromosome 1."; Genemics 10:673-680(1991).  SEQUENCE OF 890-1396 FROM N.A. SEQUENCE OF 890-1396 FROM N.A.
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PROSITE; PS01025; EGF_1; 9.

R PROSITE; PS01186; EGF_2; 6.

R PROSITE; PS50026; EGF_2; 6.

R PROSITE; PS50026; EGF_2; 6.

R PROSITE; PS50026; EGF_2; 7.

R PROSITE; PS50026; EGF_2; 1.

R PROSITE; PS01249; LAMININ_TYPE_EGF; 11.

R PROSITE; PS01209; LDLRA_1; 4.

R PROSITE; PS50068; LDLRA_2; 4.

R PROSITE; PS50026; EGA; 11.

R PROSITE; PS50026; EGF_1; EGA; 11.

R PROSITE; PS50026; EGA; 11.

R PROS
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LUL-RECEPTOR CLASS A 2.
LUL-RECEPTOR CLASS A 3.
LUL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE 1.
IAMININ EGP-LIKE 1.
IAMININ EGP-LIKE 1.
IAMININ EGP-LIKE 3.
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IAMININ EGP-LIKE 6.
IAMININ EGP-LIKE 7.
IAMININ EGP-LIKE 9.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 9.
IG-LIKE C2-TYPE 10.
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SULFATE PROTEOGLYCAN CORE PROTEIN.
InterPro; IPR003596; Ig_v.
InterPro; IPR00034; Laminin_B.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR002172; Laminin_G.
InterPro; IPR002172; LDL receptor_IPR002172; LDL receptor_Pfam; PF000082; SEA_domain.
Pfam; PF000081; EGF; 4.
Pfam; PF000082; Iaminin_BF; 7.
Pfam; PF000053; Iaminin_BF; 7.
Pfam; PF00054; Iaminin_G; 3.
                                                                                                                                                                                                                                                                                                                                                                 Probom; P0003031; Laminin B; 3.
SMART; SM00181; BGF; 15.
SWART; SM00180; BGF, Lam; 12.
SWART; SM00409; 1G5, 22.
SWART; SM00409; 1G622; 21.
SWART; SM00409; 1G622; 21.
SWART; SM00281; LamB; 3.
SWART; SM00281; LamG; 3.
SWART; SM00281; LamG; 3.
SWART; SM00281; LamG; 3.
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3687 EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI 3746
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                                                                                                                       3747 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA 3806
                                                                                                                                                                     3807 IPKAGLSSGFIGCVRELRIQGEBIVFHDLNLTAHGISHCPTCRDRPCQGGGCHDSBSSS 3866
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                                                                                                        RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA 120
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                                                        1 EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                  0; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., SaBaki M.,
           Length 4391;
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
protein precursor (HSPG) (Perlecan) (PLC).
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                                  0; Indels
       Query Match 100.0%; Score 3825; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3e-233; Matches 705; Conservative 0; Mismatches 0;
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R SWART; SW00192; LDLa; 4.

R WARRT; SW00120; SEA; 1.

R PROSITE; PS01022; SGE_1; 6.

R PROSITE; PS01026; EGF_2; 5.

R PROSITE; PS01026; EGF_3; 4.

R PROSITE; PS01248; LAMININ TYPE EGF; 11.

R PROSITE; PS01248; LDLRA 11; 4.

R PROSITE; PS01248; LDLRA 2; 4.

R PROSITE; PS01249; LDLRA 1; 4.

R PROSITE; PS01240; LDLRA 1; 4.

R PROSITE; PS01240; LDLRA 2; 4.

R PROSITE; PS01240; LDLRA 1; 4.

R PROSITE; PS01240; LDLRA 2; 4.

R PROSITE; PS01240; LDLRA 1; 4.

R PROSITE; PS01240; LDLRA 1; 4.

R PROSITE; PS01240; LDLRA 1; A.

R PROSITE; PS01240; LDRA 1; A.

R PROSITE; PS01240; LDR
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LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

IG-LIKE C-TYPE 1.

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3 (INCOMPLETE).

LAMININ EGF-LIKE 5 (C-TERMINAL).

LAMININ EGF-LIKE 5 (COMPLININ).

LAMININ EGF-LIKE 6 (N-TERMINAL).

LAMININ EGF-LIKE 7.

LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 11.

LAMININ G-LIKE C-TYPE 11.

LG-LIKE C-TYPE 11.

LG-LIKE C-TYPE 12.

LG-LIKE C-TYPE 12.

LG-LIKE C-TYPE 12.

LG-LIKE C-TYPE 13.

LG-LIKE C-TYPE 14.

LG-LIKE C-TYPE 15.

LAMININ G-LIKE 2.

LAMININ G-LIKE 1.

LAMININ G-LIKE 2.

LAMININ G-LIKE 1.

LAMININ G-LIKE 3.

LAMININ G-LIKE 1.

LG-LIKE C-TYPE 14.

LAMININ G-LIKE 14.

LG-LIKE C-TYPE 14
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BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULPATE PROTEOGLYCAN CORE PROTEIN.
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	milarity 88.6%; Score 3389.5; DB 1; Length 3707;  Conservative 33; Mismatches 40; Indels 5; Gaps 3;  Conservative 33; Mismatches 40; Indels 5; Gaps 3;  IKITERPDSADGMLLYNGQKRVPSTMLANRQPDFISFGLVGGRPEFRFDAGGGMATI 60  IKITERPDSADGMLLYNGQKRASPTWLANRQPDFISFGLVGGRPEFRFDAGGGMATI 3064  HPPPLALGGFHTYTLLRSLTGGSLIVGDLAPVNGTSQGKFGGLDLNEELYLGGYPDYGA 120  HPPPLALGGFHTYTLLRSLTGGSLIVGDLAPVNGTSQGKFGGLDLNEELYLGGYPDYGA 120  HPPPLALGGFHTYTLLRSLTGGSLIVGDLAPVNGTSQGKFGGLDLNEELYLGGYPDYGA 120  HPPPLALGGFHTYTLLRSLTGGSLIVGDLAPVNGTSQGKFGGLDLNEELYLGGYPDYGA 120  PKAGLSSGPYGGVRELRIQGSEIVFHDLALTAHGISHCFTCQDRFCQNGGCCDSESSS 180  PKAGLSSGPYGGVRELRIQGSEIVFHDVALTHGISHCFTCQDRFCQNGGCCDSESSS 180  TCVCPAGFTGSRCEHSQALHCPBACGPDATCVNRPDGRGYTCRCHLGRSGVRCEEGVT 240  TCVCPAGFTGSRCEHSQALHCHPBACGPDATCVNRPDGRGYTCRCHLGRSGVRCEEGVT 3243  TTPSKLGSGGAGSYLALPALTNTHHEIRLDVEFKPLAPDGYLLFSGGKSGPVEDFVSLAMVG 3303  HLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSOGL 360  HLEFRYELGSGLAVLRSHEPLALGRWHRVSAERLNKDGSLRVDGGRGGOVGCYDSS 420  LHTLLYLGGVEPSVPLSSPATNMSAHFRGCVGEVSVNGKRLDLITYSFLGSOGTGGCYDSS 420  LHTLLYLGGVEPSVPLSSPATNMSAHFRGCVGEVSVNGKRLDLITYSFLGSOGTGGCYDSS 3123  CEROPCOHGATCMPAGEVERQCLCRDGFKGDLCHEENPCOLREPCTRGGGCCGRCCCC 480  CHILLITH CHARACTART CHARACTA
BY SIMILARITY	BB.6%; Score 3389.5; DB 1; Lengt' 8B.9%; Pred, No. 3.6e-206; PDSADGMLLYNGQRRVPGSPTMLANRQPDF1SFGLVGGRP PDSADGMLLYNGQRRVPGSPTMLANRQPDF1SFGLVGGRP PDSADGMLLYNGQRRVPGSPTMLANRQPDF1SFGLVGGRP LGHFHTVTLLRSLTQGSL1VGNLAPVNGTSQGKFQGLDLN LGQFHTVTLLRSLTQGSL1VGNLAPVNGTSQGKFQGLDLN LGGPTTVTLLRSLTQGSL1VGNLAPVNGTSQGKFQGLDLN GGPTGCVRELRIQGSS1VGNLAPG1SHCPTCRDRPC GFTGSRCEHSQALHCHPBACGPDATCVNRPDGRGYTCRCH SGGTGCVRELRIQGSS1VGNLAPDTLTTGISHCPTCQDRPC GFTGSRCEHSQALHCHPBACGPDATCVNRPDGRGYTCRCH GGTAAAAVNTRKPCTATP-SLMADATCVNRPDGRGYTCRCH GFTAAAAVNTRKPCTATP-SLMADATCVNRPDGRGYTCRCH GGGSYLALPALTNYTHEIRLDVEFKPLAPDGYLLFSGGKS HIGH
375 388 403 403 403 403 403 403 403 403 403 403	4 · M — M   M — M   H — H   H — H   N — N   M — M   N — N   N — N   N — N   N — N
DISCULPTD	Query Match Best Local Matches 62 3006 3125 3125 3185 3185 3185 3304 33185 33185 33185 33185 33185
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initiator.

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CAUTION: It is uncertain whether Met-1, Met-18 or Met-24 is the
3484 LPGFSGPRCQQGAGXGVVESDWHPEGSGGNDAPGQXGAYFYDNGFLGLPGNSFSRSLPEV 3543
                                                               3544 PETIEFEVRISTADGLLLMQGV-VREASRSKDFISLGLQDGHLVFSYQLGSGEARLVSGD 3602
                                                                                                   3603 PINDGEWRITALREGORGSIQVDGEDLVIGRSPGPNVAVNTKDIIXIGGAPDVATLTRG 3662
         LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV 540
                                               541 PETIELEVRISTASGLILMQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSED 600
                                                                                         PINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGG 660
                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI _TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evertable Tractive explicing; Named isoforms=5; Comment=Additional isoforms seem to exist. Isoforms differ in their acetylcholine receptor clustering activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISOID SPESSOR-5; Sequence=VSP_001368;
TISOID SPECIFICITY: Embryonic inervous system and muscle.
TISOID SPECIFICITY: Embryonic inervous system and muscle.
DEVELOPMENTAL STAGE: More abundant early in development.
DINKE Contains heparan sulfate chains as well as N-linked and O-linked oilgoasccharides (By similarity).
SIMILARITY: Contains 9 Kazal-like domains.
SIMILARITY: Contains 2 laminin EGF-like domains.
SIMILARITY: Contains 1 SEA domain.
SIMILARITY: Contains 3 laminin G-like domains.
                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-1779 AND 1799-1959 FROM N.A.
TISSUB=Embryonic spinal cord;
MEDLLINE=91222570; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
"Structure and expression of a rat agrin.";
Neuron 6:811-823 (1991).
                                                                                                                                            3663 KFSSGITGCIKNLVLHTARPGAPPPQPLDLQHRAQAGANTRPCPS 3707
                                                                                                                                661 RFSSGITGCVKNLVLHSARPGAPPPOPLDLOHRAQAGANTRPCPS 705
                                                                                                                                                                                                              DSS304; Q63034;
01-MAY-1992 (Rel. 22, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                         PRT; 1959 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=P25304-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                             Agrin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R Pfeam; PF000001; Razal; 9.

R Pfam; PF00005; Razal; 9.

R Pfam; PF00005; Razal; 9.

R Pfam; PF00005; Razal; 9.

R Pfam; PF0005; Laminin_EGP; 2.

R Pfam; PF00105; Razal; 9.

R Pfam; PF00101; EGFLAMININ.

R RART; SM00180; EGF_LAMININ.

R SMART; SM00280; KAZAL; 9.

R SMART; SM00280; KAZAL; 9.

R SMART; SM0022; EGF_1; 9.

R SMART; SM0022; EGF_1; 6.

R PROSITE; PS01026; EGF_2; 1.

R PROSITE; PS01025; EGF_2; 1.

R PROSITE; PS01025; EGF_2; 1.

R PROSITE; PS01025; EGF_2; 1.

R ROSITE; PS01025; EGF_2; 1.

R RAGE EGF_2; 1.

R RAGE
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KAZAL-LIKE 2.
KAZAL-LIKE 3.
KAZAL-LIKE 4.
KAZAL-LIKE 5.
KAZAL-LIKE 6.
KAZAL-LIKE 7.
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EGF-LIKE 4.
LAMININ G-LIKE 3.
SER/THR-RICH.
SER/THR-RICH.
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EGF-LIKE 2.
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Interpro; IPR008203; RGF like.
Interpro; IPR003645; FolM.
Interpro; IPR002350; kazal
                                                                                                                                                                                                                                                                                       EMBL; M64780; AAA40703.1; -.
EMBL; M64780; AAA40702.1; ALT_INIT.
EMBL; S44194; AAB23326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003645; FolN.
InterPro; IPR002350; kazal.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000082; SEA_domain.
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HSSP; P00740; 1EDM
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1627 GALOVGDGPRVIGESP-KSRKVPHTMLNIKEPLYIGGAPDFSKLARGAAVSSGFSGVIOL 1685
                                                                                                                               1717 -----LGNPCLNGGSCVPREATYECLCPGGFSGLHCEKGL------VEKSVG 1757
                                                                                                                                                                               1758 -------DLETLAFDGRTYIEYLNAVIESELTNEIPAPETLDSRALFSEKALQSN 1805
                                                                                                                                                                                                                            394 VSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDL 453
 339 GSLRVNGGRPVLRSSPGKSQG----LNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 NDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV------PETI------
                                                                                                                                                                                                                                                              603 NDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAP--DVATLTGG
                                                                                                       454 CEHERNPCOLREPCINGGIC -- QGT - RCLCLPGFSGPRCQQGSGNGIARSDWHLEGSGG
                                                                                                                                                                                                            545 -- ELEVRISTASGILLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist. Isoforms differ in
their acetylcholine receptor clustering activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsim K.W.K., Ruegg M.A., Escher G., Kroeger S., McMahan U.J.; "cDNA that encodes active agrin.";
                                                                                                                                                                                                                                                                                                                                  1922 AYGTGFVGCLRDVVVGH-----RQLHLLEDAVTKPELRPCPT 1958
                                                                                                                                                                                                                                                                                                                   661 RESSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 705
                                                                      ||:|:||:|
|1686 VSLRGHQL-----LTQEHVLRAVDVSPFADHPCTQA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=Agrin-related protein 1;
IsoId=P31696-2; Sequence=VSP_001370;
Name=3; Synonyms=Agrin-related protein 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 26, Created)
(Rel. 26, Last sequence update)
(Rel. 41, Last annotation update)
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28-FEB-2003 (Rel.
Agrin precursor.
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01-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYG-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 -AIPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTA---HGISHC--FTCRDRPCQNGGQC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 RCEEGVTVTTPSLSGAG-----SYLALPALTNTHHEL----RLDVEFKPLAPDG 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 HDSESSSYVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPBFRPDAGSGMATIR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92; Mismatches 278; Indels 154; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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(POTENTIAL).
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/FIId=VSP 001368.
V -> VTCD (IN A VARIANT).
W; 7FEFDFDAFF89CC31 CRC64;
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1959 AA;
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                                                                                                                                                                                   Isold=P31696-3; Sequence=VSP 001369, VSP 001370;
-!- PTM: Contains heparan sulfate chains as well as N-linked and O-linked oligoaccharides (By similarity).
-!- SIMILARITY: Contains 9 Kazal-like domains.
-!- SIMILARITY: Contains 9 Kazal-like domains.
-!- SIMILARITY: Contains 1 SEA-like domains.
-!- SIMILARITY: Contains 1 SEA domain.
-!- SIMILARITY: Contains 3 laminin G-like domains.
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KAZAL-LIKB 2.
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EGF-LIKE 2.
EGF-LIKE 3.
LAMININ G-LIKE 2.
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EGF-LIKE 1.
                                                                                                                                            EMBL; M94271; AAA48585.1; -.
EMBL; M97371; AAA48586.1; -.
EMBL; M97372; -; NOT_ANNOTATED_CDS.
PIR; JH0591; AGCH.
HSSP; P00740; IEDM.
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·	25;	61 1342 120 1401 167 1455 227
•	N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). Missing (in iscoform 3). //FIGAVSP 001369. Missing (in iscoform 2 and isoform 3). //FTIGAVSP 001370. RTI = -> SIL (IN REF. 1, AAA48586). MW; B4DEBZ7C23422581 CRC64; SCOTT 796.5; DB 1; Length 1955; Pred. No. 1,38-42; Pred. No. 1,38-42; 11 indels 131; Gaps	IKITEREDSADGWLLYNGGKRVPGSFTWLANRQPDFISFGLVGGRPEFRFDAGSGWATIR
11714 11714 11714 11715 1180 11	390 659 764 161 1651 1793 131 AA, 211411 20.8%; servative	IKITERPDSADGMLLYNGQKRVPGSP
DOWAIN DOWAIN DOWAIN DOWAIN DOWAIN DOWAIN DISULFID	CARBOHYI CARBOHYI CARBOHYI VARSPLIC VARSPLIC CONFLICT SEQUENCI SEQUENCE Best Local Matches 22	2 1294 52 1343 121 1402 168
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(See http://www.isb-sib.ch/announce/
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LAMININ EGF-LIKE 2.
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LAMININ G-LIKE 2.
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LAMININ G-LIKE 1.
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modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
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BY
                                                                                EMBL; L01423, AAA49224.1; -.
PIR; T43060; T43060.
HSSP, P00740; 1EDM.
INCEPPC; IPR000152, Asx hydroxyl S.
INCEPPC; IPR000985; Cona like_lec_gl.
INCEPPC; IPR006209; EGF Z.
INCEPPC; IPR006209; EGF Z.
INCEPPC; IPR006209; EGF Z.
INCEPPC; IPR006209; EGF Z.
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FS00022; EGF_1; 5.
FS01026; EGF_2; 1.
FS50026; EGF_3; 4.
FS50025; LAM G_DOMAIN; 3.
FS50025; LAM G_DOMAIN; 3.
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                                                                                                                                                                                                                                            InterPro; IRRO02350; kazal.
InterPro; IRR002350; kazal.
InterPro; IRR00249; Laminin_G.
InterPro; IRR000082; SRA_domain.
Pfam; PP00008; EGF; 4.
Pfam; PP00059; Pazal; 2.
Pfam; PP00059; laminin_EGF; 2.
Pfam; PP00059; laminin_GG; 3.
Pfam; PP000594; laminin_G; 3.
Pfam; PP001309; SRA; 1.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 369 N-L
1328 AA; 144018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0011; EGFLAMININ.
SWART; SW00180; EGF Lam; 2.
SWART; SW00280; KAZAL; 2.
SWART; SW00280; KAZAL; 2.
SWART; SW00282; Lamid; 3.
SWART; SW002022; Lamid; 3.
PROSITE; PS00010; ASX_HYDROXY
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CARBOHYD
SEQUENCE
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    1514 MGREGEPCER---VTBQDHTMPFLPEFNGF-SYLELNGLQTLFLTCRQMSMEVVFLAKSP 1569
                                                                                                                                                                                                                                                                                                                                                                 1716 HPCTQKPNPCQ-----NGTCSPRLESYECAQRGFSGAHCEKVIIEKAAGDAEAIAFD 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                         1689 QRISIKGVPL-----KEQHIRSAVEIST------------FRA 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1770 GRIYMEYHNAVIKSPDA-------LLDYPAEPSEKALQS--NHFELSIKIEAIQG 1814
228 LGRSGLRCEEGVTVT-----TPSLSGAGSYLALPALTN---THHELRLDVEPKPLAP 276
                                                                                  277 DGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLN 336
                                                                                                                                                                   337 KDGSLRVNGGRPVLRSSPGKSQG----LINLHTLLYLGGVEPSVPLSPATNMSAHFRGCV 391
                                                                                                                                                                                                                                                   392 GEVSVNGKRIDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYERQCLCRDGFKG 451
                                                                                                                                                                                                                                                                                                                                      452 DICEHBENPCQLREPCHAGIC----QGTRCLCLPGFSGPRCQQ-----GSGHGIA-- 498
                                                                                                                                                                                                                                                                                                                                                                                                                      499 ---ESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLIWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALRE 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         616 GRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAP--DVATLIGGRFSSGIIGCVKNL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Smith M.A., Magill-Solc C., Rupp F., Yao Y.-M.M., Schilling J.W.,
Snow P., McMahan U.J.:
Snow P., McMahan U.J.:
"Isolation and characterization of a cDNA that encodes an agrin
homolog in the marine ray.";
Mol. Cell. Neurosci. 3:406-417(1992).
"I-FUNCTION: Component of the basal lamina that causes the
aggregation of acetylcholine receptors and acetylcholine-esterase
on the surface of muscle fibers of the neuromuscular junction (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Synaptic basal lamina at the neuromuscular
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Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Chondrichthyes;
Elsamobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
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--- SIMILARITY: Contains at least 2 laminin EGF-like domains.
--- SIMILARITY: Contains at least 3 EGF-like domains.
--- SIMILARITY: Contains 1 SEA domain.
--- SIMILARITY: Contains 3 laminin G-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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17.4%; Score 667; DB 1; Length 1328;
Best Local Similarity 27.0%; Pred. No. 1.2e-34;
Matches 200; Conservative 112; Mismatches 304; Indels 126; Gaps
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(GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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1099 HACTKTRNPCO-----NGGVCSPRLREYDCMCQRGFSGPQCEKA------LE-- 1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014 KGLMKINKDELVSGESPKSKKAP--HTALNLKEAFYVGGAPDFNKFARAAGIISGFTGAI 1071
                                                                                     722 SKTLIKPGNWHHVVGNRNRRSGMLSVDGEPHLIGESPPGTDGLNLDTDLFLGGTPEDEMT 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 GEVSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 DLCEHEENPCQLREPCLHGGTC----QGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGS 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 GGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEA 567
                                                                  62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYG-- 119
                                                                                                                                       120 -AIPKAGLSSGFIGCVRELRIQGEEIVFHDLN-----LTAHGISHCPT--CRDRPCQNG 170
                                                                                                                                                             GVILFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNK 337
                                                                                                                                                                                                                                                                                                                                                                                                                      338 DGSLRVW-----GGRPVLRSSPGKSQGLMLHTLLYLGGVEPSVPLSPATNMSAHFRGCV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 GQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEE 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 LVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGR----FSSGITGCVKNLVLHSARPGAP 683
                                  673 ISMEFRASNLDGLPLVQWTEKGKG----LHFYRPS-----EGYVELRFNHGVWDGVIT 721
                                                                                                                                                                                                                                                                               229 GRSGLRCE-----EGVTVTTPSLSGAGSYLALPAL---TNTHHELRLDVEFKPLAPD 277
2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A), AND FUNCTION.
MEDLINE=93339574; PubMed=8393416;
Rogalski T.M., Williams B.D., Mullen G.P., Moerman D.G.;
Products of the unc-52 gene in Caenorhabditis elegans are homologous to the core protein of the mammalian basement membrane heparan
                                                                                                                                                                                                           GQCHDSESSSYVCVCPAGFTGSRC--EHSQALHCHPEACGPDATCVNRPDGRGYTCRCHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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ID UN52 CAREL

AC Q05561, 018261, 018263; Q3XTD2; Q9XTI5;

DT 01-UN-1994 (Rel. 29, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Basement membrane proteoglycan precursor (Perlecan homolog)

GN UNC-52 OR ZC101.2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           -1- FUNCTION: Probable role in myofilament assembly and/or attachment of the myofilament lattice to the cell membrane. May be an extracellular anchor for integrin receptors in muscle.
-1- SUBGELLULAR LOCATION: Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Note=No experimental confirmation available;
--- TISSUE SPECIFICITY: Found in the basement membrane of all contractile tissues. It is concentrated over muscle dense bodies and M-lines which are associated with beta-integrin.
--- IDVELOPMENTAL STRABE: Synthesized early in embryogenesis.
--- SIMILARITY: Contains 3 LDL-receptor class A domains.
--- SIMILARITY: Contains 16 immunoglobulin-like C2-type domains.
--- SIMILARITY: Contains 3 laminin G9F-like domains.
--- SIMILARITY: Contains 3 laminin G1-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                             Percy C.M., Baynes C.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                       Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                  IsoId=Q06561~2; Sequence=VSP_007195, VSP_007196;
                                                                                                                                                                                                                                                                                 IsoId=Q06561-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                 IsoId=206561-3; Sequence=VSP_007191, VSP_007
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=4;
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InterPro; IPR008985; ConA_like_lec_gl.
                                                                                                                          REVISIONS, AND ALTERNATIVE SPLICING.
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 sulfate proteoglycan.";
Genes Dev. 7:1471-1484(1993).
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InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like
InterPro; IPR006210; IEGF.
InterPro; IPR006710; IG-1ike.
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WormPep; ZC101.2b; CE15030.
WormPep; ZC101.2c; CE15034.
WormPep; ZC101.2c; CE15034.
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                                                              STRAIN-Bristol N2;
                                              SEQUENCE FROM N.A.
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2665 RPVFIGGRHE-----PINEANDFRGIISQVVLSGHNVGLGDARIPSSVVKYDACASTNLC 2719
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1943 SQDVDL--QNLSSSGDISSCEESQFPVEEDDTTTTTTEBPRAVIRBPTTEBPTTEBPI 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 BELYLGGYPDYGAIPKAGLSSGFIGCVRBLRIQGEEIVFHDLNLTAHGISHCPTCRDRPC 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GWATIRHPIPLALGHFHTVTLLRSLTQGSLIVGDLA-----PVNGTSQGKFQGLDLN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 QNGGQCHDSBS-SSYVCVCPAGFTGSRCEHSQALHCHPBACGPDATCVNRPDGRGYTCRC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 HIGRSGLRCEEGVTVTTP-SLSGAGSYLALPALTNTHHELRLDVEFKPLAPDG----VLLF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 VNGGRPVLRSSPGKSQGLNLHTL----LYLGGVEPSVPLSPATNMSAHFRGCVGEVSVN 397
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13.4%; Score 511; DB 1; Length 3375;
Best Local Similarity 20.9%; Pred. No. 2.6e-24;
Matches 179; Conservative 140; Mismatches 332; Indels 204; Gaps
BY SIMILARITY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                3001 TEEPTEEPTTTEEPTTTEEPTTTTEEPTTTTEEPYHIYE---TSRDDDPEIIIPVETTT 3057
                                                                                                                                                                                            3058 TSTTTTSTTEEPEAEPALVLPTDPVENDVSDEEEEISTISTVSPDNGLDSDSDYSEGTL 3117
                                                                                                                                                                                                                                                                                                                                                         3118 PPDSSSEEIVVGDVYSTQEPNNICANSTC----GMNGQCVPRNMTHYTCECKLYYDGPTC 3173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3233 QMEDYISVGIVNGHLHFSYELGGGAAHLISEERVDDGKEHSVRFERKGREGQMRIDNYRE 3292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- 459
                                                                                                                                                                                                                                                                                         460 -PCQLREPCLHG-----GTCQGTRCLCLPGFSGPRCQQSGHGIAESDWHLEG-SG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                         509 GNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLHWQGVEVGEAG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          569 QCKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEMHRVTALREGRRGSIQVDGEEL 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 VSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVYNLVLHSARPGAPPQPL 688
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley, TISSUE=Brain,
MEDLINE=98360089; PubMed=9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
Nidenrification of high-molecular-weight proteins with multiple
Generalise by motif-trap screening.";
Genomics 51:27-34(1998)
-!- FUNCTION: Receptor that may have an important role in cell/cell
signaling during nervous system formation.
-!- SUBCELLULAR LOCATION: Expressed in the brain. Expressed in
cerebralum, olfactory bulb, cerebral cortex, hippocampus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain stem.

--- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.

--- SIMILARITY: Contains 9 cadherin domains.

--- SIMILARITY: Contains 8 EGP-like domains.

--- SIMILARITY: Contains 2 laminin G-like domains.

--- SIMILARITY: Contains 1 laminin EGF-like domain.

--- SIMILARITY: Contains 1 gps domain.
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28-FFB-2003 (Rel. 41, Last sequence update)

10-0CT-2003 (Rel. 42, Last annotation update)

10-0CT-2003 (Rel. 42, Last annotation update)

cadherin EGF LAG seven-pass G-type receptor 3 precursor (Multiple

celssa or MEGF2.
                                                                                                                                                ----FKGDLCEHEEN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                            449 -----
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1D CLR3_RAT

1D CLR3_RAT

28-FEB-200

DT 28-FEB-200

DT 28-FEB-200

DE Cadherin E

CELSR3 ON

CELSR3 ON

CELSR3 ON

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CELSR3 ON

CELSR3 ON

CO Enkaryota;

OC ENTARE,

CO TENEDELIC

CC -1- STINILA

CC -1- STINI
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R SWART; SW00112; CA; 9.

R SWART; SW00112; CA; 9.

R SWART; SW00112; CA; 9.

SWART; SW00112; CA; 9.

R SWART; SW00101; EGF; 6.

SWART; SW00009; Hormk; 1.

R PROSITE; SW0010; ASX HYDROXYL; 1.

R PROSITE; PS00202; EGF 2; 4.

R PROSITE; PS00202; EGF 2; 6.

R PROSITE; PS0026; EGF 2; 6.

R PROSITE; PS0026; EGF 2; 6.

R PROSITE; PS0026; EGF 2; 6.

R PROSITE; PS00669; G PROTEIN RECEP F2 2; FALSE NEG.

R PROSITE; PS00669; G PROTEIN RECEP F2 2; FALSE NEG.

R PROSITE; PS00650; G PROTEIN RECEP F2 3; 1.

R PROSITE; PS00561; G PROTEIN RECEP F2 4; 1.

R PROSITE; PS00261; G PROTEIN RECEP F2 4; 1.

R PROSITE; PS001249; LAM G DOMAIN; 2.

R PROSITE; PS001249; LAM G DOMAIN; 3.

R PROSITE; PS001249; LAM G DOMAIN; 3.

R PROSITE; PS001249; LAM G DOMAIN; 3.

R PROSITE; PS001249; LAM C DOMAIN; 3.

R PROSITE; PS001249; LAM C DOMAIN; 3.

R PROSITE; PS001249; LAM C DOMAIN; 3.

R PROSITE; PS001240; LAM C DOMAIN; 3.
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CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3.
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CALCIUM-BINDING.
CALCIUM-BINDING.
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CADHERIN 2.
CADHERIN 3.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
CADHERIN 9.
CADHERIN 9.
CADHERIN 9.
EGP-LIKE 1.
EGF-LIKE 3.
             Asx hydroxyl_S.
Cadherin.
Cond_like_lec_gl
                                                              EGF_Ca.

EGF_like.

GPCR_secretin.

horm_receptor.
                                                                                                                            Interpro; IRR002049; Laminin EGP.
Interpro; IRR001791; Laminin G.
Interpro; IRR000203; RND_cys_rich.
PEan; PF00002; 7tm 2; 1.
Pfam; PF00028; cadherin; 9.
                                                                                                                                                                                                                                        Pfam; PF00054; laminin G; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; REFLAMININ.
PRINTS; PR00249; GPCKSECRETIN.
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Pfam; PF01825; GPS; 1
Pfam; PF02793; HRM; 1
                                        .PR008985;
                                                                 PR001881;
                                                                                PR006209;
                                                                                                                     InterPro; IPR006210;
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InterPro;
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1612 GPSKDKVAVLSVDDCNVAVALRFGAEIGNYSCAAAGVQTSSKKSLDLTGPLLLGGV-PNL 1670
                                                                                                                                                                                                                                                                                                                           1712 AKSHF----CASG-----PCKNGGLCSERWGGFSCDCPVGFGKDCR 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1750 LIMAH----PYHFQGNGTLSWDFGNDMP-----------VSVPWYL 1780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1890 GPPPSSKEEG---PQGLVGCIQGVWTGFTPFGSSALPPP----SHRINVEPGCTVTNPC 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 ELEVRISTASGLLLWQGVEVG-----EAGQGKDFISLGLQDGHLVFRYQLGSGEARLV 597
                                                         295 SLAMYGGHLEFRYELGSGLAVLRSAEP--LALGRWHRVSAERLNKDGSLRVNGGRPVLRS 352
                                                                                                                                                                        353 SPGK----SQGLNLHTLLYLGGVEPSV 375
                                                                                                                                                                                                                                                                                        376 PLS-PATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSSFCERQPCQHGATCM 434
                                                                                                                                                                                                                                                                                                                                                                                                           435 PAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQ----GTRCLCLPGFSGPRCQ 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 QGSGHGIAESDWHLEGSG-----GNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650 GAPDVATLIGGRFSSGIIGCVKNLVLHSARPGA---PPPQPLDLQHR--AQAGAN-TRPC 703
                                                                                                         1557 ALELVAGOVRLTYSTGESSTVVSPTVPGGLSDGOWHTVHLRYYNKPRTDALGGAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 SEDPINDGEWH--RVTALRE--GRRG----SIQVDGEELVSGRSPGPNVAVNAKGSVYIG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Missler M., Hammer R.E., Suedhof T.C.;
"Neurexophilin binding to alpha-neurexins. A single LNS domain
"Unctions as an independently folding ligand-binding unit.";
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STRAIN-Sprague-Dawley, TISSUE-Brain;
MEDLINE-92320296; PubMed-1621094;
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1D NXZA_RAT

AC 063374; 063375;

C 263374; 063375;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Newtexin 2-alpha precursor (Newtexin II-alpha).
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MEDLINE=95209856; PubMed=7695896;
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87; Mismatches 256; Indels 252; Gaps
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EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 2.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
LAMININ EGF-LIKE.
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Missing (in some isoforms Alpha 3B).
Frid=VSP 003514.
Missing (in some isoforms Alpha 4B).
Frid=VSP 003515.
Missing (in some isoforms Alpha 5B).
Frid=VSP 003515.
DEGSYQVDQSRNYISNSAQSNGAVVKEKAPAAPKTPSKAKK
NKDKEYYV -> CRKSPREKLIPGSAQGIGLDLAAACCVC
RCRATCIAGKPLEERGGGREGGERGMQIYIKNK (in some isoforms Alpha 6).
Frid=VSP_003517.
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Best Local Similarity 21.6%; Pred. No. 5.9e-19;
Matches 193; Conservative 114; Mismatches 274; Indels 312; Gaps
                                                                                                                                                                  Missing (In some isoforms Alpha 2C).
/FITd=VSP 003511.
Missing (In some isoforms Alpha 2B).
/FITd=VSP 003512.
DCLRVGCAPS -> G (in some isoforms Alpha
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/FILE-VSP 003509.
Missing (in some isoforms Alpha 1C)
/FILE-VSP_003510
                                                                              C. . .) (POTENTIAL).
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1715 AA; 185282 MW; 59FBF18661F3DB15 CRC64;
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312 GLAVIR--SAEPLALGRWHRVSAER-INKDGSLRVNGGRPVIRSSPGKSOGINTHTLLYL 368
                                                                                                                                                  369 GGVEPSVPLSPATNMSAH---FRGCVGEVSVNGKRLDLTYSFLGSQGIGQCY----DSS 420
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Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
"The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22158633; PubMed-12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1272 YRLGRVVDEWLLDKGRQLTIFNSQAAIKIGGRDQ-----GRPFQGQVSGLYYN 1319
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Rowen L., Madan A., Qin S., Baradarani L., Birditt B., Bloom S.,
Burke J., Dors M., Fleetwood P., Kaur A., Madan A., Nesbitt R.,
Pate D., Hood L.,
"Sequencing of human neurexin II gene.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
Seki N., Yoshikawa T., Azuma T., Muramatsu M., Saito T.,
"Human neurexin II.";
Submitted (NOV-1999) to the EMBL/Genbank/DDBJ databases.
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Q9P25Z; OSY2D6;
Q9P25Z; OSY2D6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
NEUTEXID 2-alpha precursor (Neurexin II-alpha).
NRXN2 OR KIAA0921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 272-1712 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
NX2A_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 6:63-70(1999).
-!-! FUNCTION: Neuronal cell surface protein that may be involved in
cell recognition and cell adhesion. May mediate intracellular
                                                                                                                                                                                                       Event=Alternative promoter;

Comment=A number of isoforms, alpha-type (shown here) and
beta-type (AC P58401), are produced by use of alternative
promoters promoters isoforms differ from alpha-type isoforms
in their N-terminus;
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; IPR008985; ConA like_lec_gl.

R InterPro; IPR008209; EGF like.

R InterPro; IPR008209; EGF like.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR001895; Neurexin_like.

R Pfend; PP00008; EGF; 3.

R SMART; SM00184; Laminin_G; 5.

R SMART; SM00184; Laminin_G; 5.

R SMART; SM00182; EGF_1; FALSE_NEG.

R PROSITE; PS00186; EGF_2; PALSE_NEG.

R PROSITE; PS00186; EGF_2; PALSE_2; PAL
                                                                           signaling.
-!- SUBUNIT: The laminin G-like domain 1 binds to neurexophilin 1.
Specific isoforms bind to alpha-dystroglycan (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                            ISOId=QPF262-1, ~~;-
Name=2; Synonyms=Abpha-2B;
ISOId=Q9P282-2; Sequence=VSP_003505, VSP_003507,
VSP_003508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- TISSUE SPECIFICITY: Predominancly expressed in brain.
-1- SIMILARITY: Contains 6 laminin G-like domains.
-1- SIMILARITY: Contains 3 EGF-like domains.
-1- SIMILARITY: Belongs to the neurexin family.
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMININ G-LIKE 1.
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LAMININ G-LIKE 3.
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LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMININ G-LIKE 6.
                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9P2S2-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB035266; BAA94075.1; -.
EMBL; AC044790; AAK68154.1; -.
EMBL; AB023138; BAA76765.2; ALT_INIT.
HSSP; QG3373; 1C4R.
GGREW; HSNC:8009; NEXNZ.
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1712
1636
1657
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242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 EPSVPLSPATNMSAH---FRGCVGEVSVNGKRLDLTYSFLGSQGIGQCY----DSSPCE 423
                                                                                                                                    37;
                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                                                                                                               LPALTNITHHELRLDVEFKPLAPDGVILFSGGKSGPVEDFVSLAMVGGHLBFRYBLGSGLA 314
                                                                                                                                                                                                                                                                                                                                                                                                              986
                                                                                                                                                                                                                                                                                                                                                                                                                                371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROPCOHGATCMPAGEYEFOCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPG 483
                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                         753
                                                                                                                                                                                                                                                                                                                                                                            874 VPSNFIGHLSGLVFNGOPYMDQCKDGDITYCELNARFGLRAIVADPVTFKSRS---SYLA 930
                                                                                                                                                                    576
                                                                                                                                                                                                     634
                                                                                                                                                                                                                                        694
                                                                                                                                                                                                                                                         ----HSOA 199
                                                                                                                                                                                                                                                                                          ----- 210
                                                                                                                                                                                                                                                                                                          EDVSLRFMSQRAYGLMWATTSRESADTLRLELDGGQMKLTVNLDCLRVGCAPSKGPETLF 813
                                                                                                                                                                                                                                                                                                                                            814 AGHKLINDNEWHTVRVVRRGKSLQLSVDNVTVEGQMAGAHMRLEFHNIETGIMTERRFISV 873
                                                                                                                                                                                                                                                                                                                                                             ------DGRGYTCRCHLG------RSGLRCEEGVTVTTPSLSGAGSYLA 254
                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                        484 FSGPRCQQ-----GSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                315 VLR--SAEPLALGRWHRVSAER-LNKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 VSEDP---INDGEWHRVTALREGRRGSIQVD----GEELVSGRSPGPNVAV-----
                                                                                                                                                                                                                                                                    RASSRKVNDGEWCHVDFQRDGRKGSISVNSRSTPFLAT--GDSBILDLESELYLGGLPEG
                                                                                                                                                                                                                                 2 IKITFRPDSADGMLLYN-GQKRVPGSPTWLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                              RHPT-PLALGHFHTVTLLRSLTQGSLIVGDLA-PVNGTSQGKFQGLDLNEBLYLGGYPDY
                                                                                                                                                                                                                       GAIP------KAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCP-----TC
                                                                                                                                    Indels 309; Gaps
                                                                                                                   DB 1; Length 1712;
      N-LINKED (GLCNAC. .) (POTENTIAN LINKED (GLCNAC. .) (POTENTIAN LINKED (GLCNAC. .) (POTENTIAN LINKED (GLCNAC. .) (POTENTIAN LINKED (In isoform 2).

/FIIdavSP 003505.
/FIIdavSP 003506.

/FIIdavSP 003506.

/FIIdavSP 003506.
                                                                                          /FTId=VSP 003508.
MW; E4E8EC404DA1D0B0 CRC64;
                                                                                                                                                                                                                                                         RDRPCONGGOCHDSESSYVCVC-PAGFTGSRCE------
                                                                                (in isoform 2).
                                                                                                                                     Conservative 114; Mismatches 275;
(GLCNAC. .
                                                                                                                    11.0%; Score 420.5; DB 1
21.6%; Pred. No. 6.3e-19;
                                                                         003507.
                                                                          /FTId=VSP
                                                                                   Missing
                                                                                                                                                                                                                                                                                                                             -------ATCVNRP-----
                                                                                                   1712 AA; 184980
                                                                                   1282
                                                 399
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                                                                                                                            Similarity
                                                                                  1253
                                                 393
                                                                   797
                                                                                                                                     192;
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        CARBOHYD
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CARBOHYD
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ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comment=A number of isoforms are produced by use of alternative promoters. The alpha and beta (AC P58400) isoforms differ in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; The coding sequences of unidentified human genes. IX The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                     GRVVDEWLLDKGRQLTIFNSQAAIKIGGRDQ-----GRPFQGQVSGLYYN 1316
----NAKGSVYIGGAPDVATLTGGRFSSGITGCVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seki N., Yoshikawa T., Azuma T., Saito T., Muramatsu M.; "Human neurexin I-alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 441-1121 FROM N.A.
Mead K., Wohldmann P., Minges B.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   NXIA HUMAN STANDARD; PRT; 1477 AA.
QQULĒI; O60323; Q9C079; Q9C080; Q9C081; Q9H3M2; Q9UDM6;
28-FEB-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Neuraxin 1-alpha precursor (Neurexin I-alpha).
NRXNI OR KIAA0578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing, Named isoforms=1;
Comment=A number of isoforms may be produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....soid-egoulb1-1; Sequence=Displayed;
-!- TISSUE SPECIFICITY: Heart and brain.
-!- PTM: N- and O-glycosylated (By similarity);
-!- SIMILARITY: Contains 6 laminin 6-like domains.
-!- SIMILARITY: Contains 3 EGF-like domains.
-!- SIMILARITY: Belongs to the neurexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=98290545; PubMed=9628581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1083-1477 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 105-1477 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissuE=Brain
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                                                                    1272
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1066 ----ISDALFCN------GQIE------RG--CEGPSTTCQ-EDSCSNQ 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963 HYVFDLGNGANLIKGSSNKPLNDNQWHNVMISRDTSNLHTVKIDTKITTQITAG----- 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          651 -----APDVATLIGGRESSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANIRPCP 704
                                                                                                                                                                                                                                                                                                             912 KS-----SXVALATL-QAYTSWHLFFQFKITSLDGLILYN---SGDGNDFIVVELVKGYL 962
                                                                                                                                                                                                                                                                                                                                                                             304 BFRYELGSGLAVLR--SAEPLALGRWHRVSAER-----LUNKDGSLRVNGGRPVLRS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 YFHDDGFLAFPGHVFSRSLPEVPETIELE---VRTSTASGLLLWQGVEVGEAGQGKDFIS 575
                                                                                                                                                                                        243
                                                                                                                                                                                                                                      911
                                        732 PVVMHTEAEDVSLRFRSQRAYGILMATTSRDSADTLRLELDAGRVKLTVNLDCIRINCNS 791
                                                                                                                                          851
  207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 IGLODGHLVFRYOLGSGEARLVSEDP-INDGEWHRVTALREGRRGSIQVDGEELVSGRSP
                                                                                                                                                                                                                                   852 ITERRYLSSVPSNFIGHLOSLTFNGMAYIDLCKNGDIDYCELNARFGFRNIIADPVTFKT
                                                                                                                                                                                                                                                                                    244 PSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 SPGKSQGLNLHTLLYLGGV--EPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 QGIQQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 GTC----QCTRCLC-LPGFSGPRCQQ------GSGHGIAESDWHLEGSGGNDAPGQYGA
                                                                                                                                       792 SKGPETLFAGYNLNDNEWHTVRVVRRGKSLKLTVDDQQAMTGQMAGDHTRLEFHNIETGI
                                                                                                                                                                                        ----CHL-GRSGLR--CEEGVIVII
----LHCHPEAC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
VCBI_TaxID=9913;
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Ullrich B., Ushkaryov Y.A., Suedhof T.C.;
"Cartography of neurexins: more than 1000 isoforms generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1150 ---DRLAIGF-----STVOKEAVLVRVDSSGL
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2004 (Rel. 43, Last annotation update)
Neurexin 1-alpha precursor (Neurexin I-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
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  ----HSQA-----
                                                                                                   --GPDATCV--NRPDGRGYTCR
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          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                     R InterPro; IPR000152; Asx hydroxyl_S.
R InterPro; IPR000152; Asx hydroxyl_S.
R InterPro; IPR000520; EGF_Iike.
R InterPro; IPR000520; EGF_Iike.
R InterPro; IPR000520; EGF_Iike.
R InterPro; IPR000526; Neurexin-like.
R Pfam; PF00008; EGF; S.
R Pfam; PF00008; EGF; S.
R SWART; SM00294; Laminin G; 6.
R PROSITE; PS00020; EGF_3; S.
R PROSITE; PS00020; EGF_3; Allose NEG.
R PROSITE; PS00020; EGF_
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10.8%; Score 412.5; DB 1; Length 1477;
Best Local Similarity 20.8%; Pred. No. 1.7e-18;
Matches 200; Conservative 113; Mismatches 287; Indels 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161882 MW; FF845FB428BIA683 CRC64;
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(GLCNAC. . .)
(GLCNAC. . .)
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LAMININ G-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-ALA.
N-LINKED (GLCNAC. . .)
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LAMININ G-LIKE 3.
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LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
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LAMININ G-LIKE 6.
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                    entities requires a license agreement (
or send an email to license@isb-sib.ch)
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                                                                                    EMBL, AB035356, BAA87821.1; --
EMBL, ABA21150, BAA2504.1; --
EMBL, AC007462; AAC5336.1; --
EMBL, AC068725, AAC59602.1; --
EMBL, AC068725, AAC59602.1; --
EMBL, AC078994; AAC4520.1; --
EMBL, AC078994; AAC59642.1; --
                                                                                                                                                                                                                                                        HSSP; Q63373; 1C4R.
Genew; HGNC:8008; NRXN1.
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1477 AA;
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CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is a long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms=12;
Comment-Additional isoforms seem to exist. There is probably comment-Additional isoforms seem to exist. There is a cambination of five more than 96 isoforms. There is a combination of five alternatively spliced domains at sites 1 to 5, each consisting of modular sequences (A-G) that seem to be used independently. For splice site 1 additional splice modules might be possible thus increasing the number of possible isoforms. Beta isoforms (AC Q28142) share the combination of two alternatively spliced domains at sites 4 and 5. Experimental confirmation may be lacking for some isoforms:
alternative splicing and expressed in distinct subsets of neurons."; Neuron 14:497-507(1995).
                                                                                                                                                                                                       "Structure and evolution of neurexophilin.";
J. Neurosci. 16:4360-4369(1996).
-!- FUNCTION: Neuronal cell surface protein that may be involved in
cell recognition and cell adhesion. May mediate intracellular
                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: The cytoplasmic C-terminal region binds to CASK. Binds SYTL1. Laminin G-like domain 2 binds to NXPH1. Isoforms 9 and alpha-4c bind to alpha-dystroglycan. Isoform alpha-4c binds to alpha-latroxin (By similarity).
-!- SUBCELLULAR LOCATION Type I membrane protein (Potential).
                                                                                                                MEDLINE=96285495; PubMed=8699246;
Petrenko A.G., Ullrich B., Missler M., Krasnoperov V., Rosahl T.W.,
Suedhof T.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Event=Alternative promoter;
Comment=A number of isoforms, alpha-type (shown here) and
beta-type, are produced by use of alternative promoters.
Beta-type isoforms differ from alpha-type isoforms in their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2; Synonyms=Alpha=1B;
Isoid=Q28146-1; Sequence=VSP_003478;
Isoid=Q28146-3; Sequence=VSP_003478;
Name=3; Synonyms=Alpha=1B;
Name=3; Synonyms=Alpha=1B;
Isoid=Q28146-3; Sequence=VSP_003474;
Name=5; Synonyms=Alpha=1B;
Isoid=Q28146-4; Sequence=VSP_003477;
Name=5; Synonyms=Alpha=1B;
Isoid=Q28146-6; Sequence=VSP_003474, VSP_003477;
Name=5; Synonyms=Alpha=1B;
Isoid=Q28146-6; Sequence=VSP_003476, VSP_003478;
Name=6; Synonyms=Alpha=1B;
Isoid=Q28146-7; Sequence=VSP_003476, VSP_003478;
Name=8; Synonyms=Alpha=2B;
Isoid=Q28146-7; Sequence=VSP_003480;
Isoid=Q28146-9; Sequence=VSP_003481;
Name=1; Synonyms=Alpha=3B;
Isoid=Q28146-11; Sequence=VSP_003481;
Name=11; Synonyms=Alpha-4B;
Isoid=Q28146-11; Sequence=VSP_003481;
Name=12; Synonyms=Alpha-4B;
Isoid=Q28146-12; Sequence=VSP_003481;
Name=12; Synonyms=Alpha-4B;
Isoid=Q28146-12; Sequence=VSP_003481;
Name=12; Synonyms=Alpha-4B;
Isoid=Q28146-12; Sequence=VSP_003482;
Isoid=Q28146-12; Sequence=VSP_003482;
Isoid=Q28146-12; Sequence=VSP_003481;
Synonyms=Alpha-5B;
Isoid=Q28146-12; Sequence=VSP_003481;
Isoid=Q28146-11; Sequence=VSP_003481;
Isoid=Q2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1; Synonyms=Alpha-1A2A3A4A5A;
IsoId=Q28146-1; Sequence=Displayed;
                                                                                                      INTERACTION WITH NEUREXOPHILIN
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PIR, 145944; 145944.
HSSP; Q63373; 1C4R.
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Best Local Similarity 20.5%; Pred. No. 4.9e-18;
Matches 203; Conservative 112; Mismatches 285; Indels 391; Gaps
                                                                                                                                                     R PHEM; FFUNDS:

R SMART; SM00294; 4.lm; I

R SMART; SM00181; EGF; 2.

SMART; SM00182; EGF; 2.

SMART; SM00182; EGF; 2.

R PROSITE; PS001186; EGF 2; FALSE_NEG.

PROSITE; PS001186; EGF 2; FALSE_NEG.

PROSITE; PS50025; LAM_G DOMAIN; 6.

BR SIGNAL; Transmembrane; Repeat, Cell adhesion; EGF-like domain;

KW Signal; Transmembrane; Repeat, Cell adhesion; EGF-like domain;

KW Signal; Transmembrane; Repeat, Cell adhesion; EGF-like domain;

KW SIGNAL

SI 11530 NEURENIN:

FT CHAIN

31 1454 ELEMANTARIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FIId=VSP_003477.
Missing (in isoform 2, isoform 3 and isoform 6).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Missing (in isoform 3 and isoform 5)
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Missing (in isoform 9).
FYTGEVSP 003479.
Missing (in isoform 8).
/FITGEVSP 003480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /IBBilly
/FrId=VSP 003474.
Missing (in isoform 7).
/*mrA=VSP_003475.
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LAMININ G-LIKE 1.
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LAMININ G-LIKE 3.
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LAMININ G-LIKE 5.
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LAMININ G-LIKE 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 2.
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Asx hydroxyl S.
Cona like lec_gl.
EGF_like.
                                Interpro; IPR006209; EGF like.
Interpro; IPR006210; IEGF.
Interpro; IPR001791; Laminin G.
Interpro; IPR001891; Neurexin-like.
Pfam; PP00008; EGF; 2.
Pfam; PP00054; Iaminin G; 6.
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binding.
SIMILARITY: Contains 6 laminin G-like domains
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IsoId=Q63372-1; Sequence=Displayed;
TISSUE SPECIFICITY: Brain (neuronal s)
                                                                                                                                                                                                                                                                                                                                                                                                                      Bites 4 and
                                                                                                                                                                                                                               N-terminus;
signaling
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
(Neurexin I-alpha)
                                                                                                                                                                                                                                                                                                                                                                                  1514 AA
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XAT RAT NX1A RAT Q63372; 28-FEB-2003 15-MAR-2004

NRXN1.

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TISSUE SPECIFICITY: Brain (neuronal synapse).
PTM: N- and O-glycosylated (By similarity).
MISCELLANEOUS: Alpha-latroxin competes with alpha-dystroglycan for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evert=Alternative, in the splicing, Named isoforms=1, Comment=Alternative Splicing, Named isoforms may be produced by alternative Comment=At least 96 isoforms may be produced by alternatively spliced applicing. There is a combination of five alternatively spliced domains at sites 1 to 5, each consisting of modular sequences (A-G) that seem to be used independently. For splice site 1 additional splice modules might be possible thus increasing the number of possible isoforms. Beta-type isoforms (AC Q63373) share the combination of two alternatively spliced domains at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBBURT: Binds SYTL1 (By similarity). The cytoplasmic C-terminal region binds to CASK. Laminin G-like domain 2 binds to NXPH1 and NXPH3. Isoforms alpha 2C and alpha 4C bind to alpha-dystroglycan. Isoforms alpha 4C bind to alpha-latroxin.
-1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECTION WITH NEUREXOPHILINS 1 AND MEDLINE=99074239; PubMed=9856994; Missler M., Hammer R.E., Suedhof T.C., Missler M., Hammer R.E., Suedhof T.C., Flammer R.E., Suedhof T.C., Flammer R.E., Suedhof T.C., Flammer R.E., Suedhof T.C., J. Hammer R.E., Suedhof T.C., J. Single INS domain functions as an independently folding ligand-binding unit."; J. Biol. Chem. 273:34716-34723 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative promoter;
Comment-A number of laoforms, alpha-type (shown here) and
beta-type, are produced by use of alternative promoters.
Beta-type isoforms differ from alpha-type isoforms in their
                                                                                  Ushkaryov Y.A., Petrenko A.G., Geppert M., Suedhof T.C., "Neurexins: synaptic cell surface proteins related to the alphalarrotoxin receptor and laminin.", Science 257:50-56(1992).
                                                                                                                                                                                                                                         ζ
                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=95209856; PubMed=7695896;
Ullrich B., Ushkaryov Y.A., Suedhof T.C.;
"Carticgraphy of neurexins: more than 1000 isoforms generated alternative splicing and expressed in distinct subsets of neu Neuron 14:497-507(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99211386; PubMed=10197529;
Sugite S., Khvochtev M., Suedhof T.C.;
"Neurexins are functional alpha-latrotoxin receptors.";
Neuron 22:489-496(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH CASK.
MEDLINE=96256685; PubMed=8786425;
Hata Y., Butz S., Suedhof T.C.;
"CASK: a novel dlg/PSD95 homolog with an N-terminal calmodulin-dependent protein kinase domain identified with neurexins.";
                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH ALPHA-LATROTOXIN.
                                                                      MEDLINE=92320296; PubMed=1621094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurosci. 16:2488-2494(1996).
  WCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCIRINCNSS -> G (in some isoforms Alpha
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (in some isoforms Alpha IC).
MISSING (in some isoforms Alpha IC).
Missing (in some isoforms Alpha IG).
                                                                                                                                                                                                                                                          R InterPro; IPR00095; Asx hydroxyl S.
R InterPro; IPR000152; Asx hydroxyl S.
R InterPro; IPR000859; Cond_like_lee_gl.
R InterPro; IPR006209; EGF_like.
R InterPro; IPR00159; Laminin G.
R InterPro; IPR00159; Neurexinin G.
R InterPro; IPR00159; Neurexinin G.
R InterPro; IPR00154; Laminin G, S.
Pfam; PF00008; EGF; 2.
R SWART; SW00181; EGF; 3.
R PR051TE; PS001022; EGF 2; FALSE_NEG.
R PR051TE; PS001025; LAM G DOWAIN; 6.
R PR051TE; PS0022; EGF 2; FALSE_NEG.
R PR051TE; PS0022; LAM G DOWAIN; 6.
R PR051TE; PS0022; LAM G DOWAIN; 6.
R SIGNAL Alternative promoter usage.
R SIGNAL Alternative promoter usage.
R SIGNAL ALTERNATIVE STATES STAT
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/Frid=VSP 003489.
Missing (In some isoforms Alpha 2B).
/Frid=VSP 003490.
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Missing (In some isoforms Alpha 5B) /FIIdavSp 003493.
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EXTRACELLULAR (POTENTIAL)
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LAMININ G-LIKE 1.
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LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
-i- SIMILARITY: Contains 3 EGF-like domains.
-i- SIMILARITY: Belongs to the neurexin family.
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LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
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                                                                 2 IKITFRPDSADGMLLY-NGOKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                             Matches 202; Conservative 113; Mismatches 285; Indels 391; Gaps
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RESULT 13 CLR3\_MOUSE

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DR PROSITE; PS00022; EGF_1; 5.

DR PROSITE; PS0186; EGF_1; 5.

DR PROSITE; PS0186; EGF_1; 6.

DR PROSITE; PS018649; G_PROTEIN RECEP_F2_1; FALSE_NEG.

DR PROSITE; PS00650; G_PROTEIN RECEP_F2_2; FALSE_NEG.

DR PROSITE; PS00551; G_PROTEIN RECEP_F2_2; 1.

DR PROSITE; PS0021; G_PROTEIN RECEP_F2_4; 1.

DR PROSITE; PS0021; GFS; 1.

DR PROSITE; PS0025; LAM G_DOMAIN; 2.

RROSITE; PS01248; LAM G_DOMAIN; 2.

RROSITE; PS01248; LAMININ_TYPE_EGF; 1.

W EGP_1ike domain; Calcium-binding; Laminin EGF-1ike domain; Repeat;

M Developmental protein; Hydroxylation;

T SIGNAL
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CADHERIN 4.
CADHERIN 6.
CADHERIN 6.
CADHERIN 7.
CADHERIN 7.
CADHERIN 7.
CADHERIN 8.
CADHERIN 8.
CADHERIN 8.
CADHERIN 9.
CADHERIN 9.
CALLIKE 1, CALCIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
EGF-LIKE 4, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000832; GPCR secretin.
InterPro; IPR001879; hormn_receptor.
InterPro; IPR00210; IEGF.
InterPro; IPR002049; Laminin BGP.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
Fami, PF001021; Trm 2; 1.
PF001021; Trm 2; 1.
                                                                                                               Fram; Pro0008; EGF; 5.

Fram; Pro1825; GRF; 5.

Fram; Pro1823; HRR; 1.

Fram; Pro1823; HRR; 1.

Fram; Pro1823; HRR; 1.

Fram; Pro1823; HRR; 1.

Fram; Pro1824; Haminin_G; 2.

FRINTS; PR01829; GRCKSECRETIN.

FRINTS; PR01829; GRCKSECRETIN.

SMART; SM0112; CA; 9.

SMART; SM0181; EGF; 6.

SMART; SM0181; EGF; 6.

SMART; SM01829; Lamk; 1.

SMART; SM01829; Lamk; 1.

FR0181E; PS0181; CADHERIN 1; 7.

FR0181E; PS0181; CADHERIN 1; 7.

FR0181E; PS0181; CADHERIN 1; 7.
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                                                                                                                                                                                             STRAIN=C57BL/6;
MEDLINE=2183555; PubMed=11850187;
MISSIT F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.;
"Developmental expression profiles of Celsr (Flamingo) genes in the mouse.";
                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 2574-3046 FROM N.A., AND DEVELOPMENTAL STAGE.
MEDLINE=21534880; PubMed=11677057;
Formstone C.J., Little P.F.R.;
"The flamingo-related mouse Celsr family (Celsrl-3) genes exhibit distinct patterns of expression during embryonic development.";
Mech. Dev. 109:91-94 (2001).
                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                  0915170; 09ESDD;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 3 precursor.
CELSR3.
                                                                                                                                                                              SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGES.
         PRT; 3301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1858236; Celsr3.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR002126; Cadherin.
InterPro; IPR008985; ConA_like_lec_gl.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF427498; AAL25099.1; -.
EMBL; AF188752; AAG17057.1; ALT_FRAME.
                                                                                                                                                                                                                                                                   Mech. Dev. 112:157-160(2002).
         STANDARD;
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545 ELEVRISTASGLILWQGVEVG-----BAGQGKDFISLGLQDGHLVFRYQLGSGBARLV 597
                                                                                                                                                                                                                                                                                                     598 SEDPINDGEWH--RVTALRE--GRRG----SIQVDGEELVSGRSPGPNVAVNAKGSVYIG 649
            ---SQGLNLHTLLYLGGVEPSV 375
                                                                                                                                                                                                                                                                                                                                                                               650 GAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQPLDLQHRAQAGAN-TRPCPS 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 PLS-PATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCM
                                                                                                                         435 PAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQ----GTRCLCLPGFSGPRCQ
                                                                                                                                                                                  491 QGSGHGIAESDWHLEGSG-----GNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-99033071; PubMed-9813312;
Itoh A., Miyabayashi T., Ohno M., Sakano S.;
"Cloning and expressions of three mammalian homologues of Drosophila
slit suggest possible roles for slit in the formation and maintenance
of the nervous system.";
Brain Res. Mol. Brain Res. 62:175-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Distinct but overlapping expression patterns of two vertebrate slit homologs implies functional roles in CNS development and organogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holmes G.P., Negus K., Burridge L., Raman S., Algar B., Yamada T.,
Little M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2), SEQUENCE OF 1122-1129, FUNCTION. SUBUNIT, AND SUBCELLULAR LOCATION.
TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY TISSUE-Fetal lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTENCE FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY TISSUE=Petal brain, and Petal kidney;
MEDLINE=99279238; PubMed=10349621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLT2 HUMAN STANDARD; PRT; 1529 AA. 10-07-2003 (Rel. 42, Last sequence update) 10-07-2003 (Rel. 42, Last sequence update) 10-07-2003 (Rel. 42, Last sequence update) 10-07-2003 (Rel. 42, Last annotation update) Slit homolog 2 protein precursor (h-Slit-2). Homo sapiens (Human)
                                                                                                                                                        1710 AKSHF-----CASG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFLSPL-LGHFLEGVAAVLATPTEDVFIFNIQNDIDVGGTVLNVSFSALAP-RGAGAGAA 1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 SSSYVCVCPAGFIGSRCE-HSQALHCHPEACGPDATCVNRPDGRGYICRCHLGRS--GLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEEGVIVIIPSLSGAGSYLALPALINTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1.7e-17;
91; Mismatches 263; Indels 244; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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3301 AA; 358455 MW; A6B18F2DF7F4DEBG CRC64;
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Matches 179; Conservative
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LRR 20.
    PROSITE; PSS0026; EGF_3; 9.
PROSITE; PS01187; EGF_GA; 2.
PROSITE; PSS0025; LAM_G_DOMAIN; 1.
Neurogenesis; Glycoprofein; Signal; Alternative splicing; EGF-like domain; Repeat; Leucine-rich repeat.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
Name=3;
Isold=04813-3; Sequence=VSP 050036;
Isold=0494813-3; Sequence=VSP 050036;
TISSUE SPECIFICITY: Fetal lung and kidney, and adult spinal cord.
Weak expression in adult adrenal gland, thyroid, trachea and other
tissues examined.
SIMILARITY: Contains 7 EGF-like domains.
SIMILARITY: Contains 13 leucine-rich (LRR) repeats.
SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
SIMILARITY: Contains 1 laminin G-like domain.
                                                                                                                                                                                                                   Isold=094813-2; Sequence=VSP_050035, VSP_050036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB017168; BA2538511; ---
EMBL; AB017168; BA2538511; ---
EMBL; AF133270; AAD25539.1; ---
HSSP; P00744; LCCF.

GENEW, HGNC111086; SLITZ.

MIM; 60374; LCCF.

GO; GO:0005557; C:extracellular; IEP.

GO; GO:0005515; F:chemorepellant activity; IMP.

GO; GO:0005515; F:chemorepellant activity; IMP.

GO; GO:0005515; F:chemorepellant activity; IMP.

GO; GO:0005515; F:protein binding; TAS.

GO; GO:0005515; F:protein binding; TAS.

GO; GO:0007509; P:meedocar migration; IMP.

GO; GO:0007509; P:meedocar migration; IMP.

GO; GO:0007509; P:meedocar migration; IMP.

GO; GO:0007509; P:meerogenesis; TAS.

InterPro; IPR000121; Asx hydroxyl S.

InterPro; IPR001791; Laminin G.

InterPro; IPR001791; LRR. Cterm.

InterPro; IPR0001791; LRR. Ct
                                                                                                                                                 Name=1;
IsoId=094813-1; Sequence=Displayed;
Name=2;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple
"I EGF-like motifs by motif-trap screening.";
"EGF-like motifs by motif-trap screening.";
"Genomics 51:27-34(1998).
"I Genomics 51:27-34(1998).
"I SIMILARITY: Receptor that may have an important role in cell/cell
signaling during nervous system formation.
"I SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
"I SIMILARITY: Contains 9 cadherin domains.
"I SIMILARITY: Contains 9 EGF-like domains.
"I SIMILARITY: Contains 1 laminin GF-like domain.
"I SIMILARITY: Contains 1 laminin EGF-like domain.
"I SIMILARITY: Contains 1 laminin EGF-like domain.
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R PROSITE; PSCO0022; EGF 1; 6.

R PROSITE; PSCO0024; EGF 2; 6.

R PROSITE; PSCO064; EGF 3; 6.

R PROSITE; PSCO064; EGF 3; 6.

R PROSITE; PSCO0650; GPROTEIN RECEP F2 1; FALSE NEG.

R PROSITE; PSCO027; GPROTEIN RECEP F2 3; 1.

R PROSITE; PSCO027; GPROTEIN RECEP F2 3; 1.

R PROSITE; PSCO025; LAM G DOMAIN; 2.

R PROSITE; PSCO026; Transmembrane; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat; PSCO011; Hydroxylation; Signal.
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CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3.
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InterPro; IPR00125; Asa hydroxyl_S.
InterPro; IPR00126; Cadherin.
InterPro; IPR00126; Cadherin.
InterPro; IPR00132; Gadherin.
InterPro; IPR00142; EGF_Z.
InterPro; IPR00142; EGF_Z.
InterPro; IPR001831; EGF_R.
InterPro; IPR001832; GPCR_Secretin.
InterPro; IPR001832; GPCR_Secretin.
InterPro; IPR001873; Horm.receptor.
InterPro; IPR001873; Laminin_G.
InterPro; IPR001973; Laminin_G.
InterPro; IPR001971; Laminin_G.
InterPro; IPR001031; EGF; S.
InterPro; IPR001031; EGF; S.
InterPro; IPR001031; GGF; S.
InterPro; IPR001031; GGF; S.
InterPro; IPR001031; GGF; S.
InterPro; IPR00112; GGF; S.
InterPro; IPR00113; EGF; S.
INTS; PR00112; EGF; S.
INTS; PR00112; EGF; S.
INTS; RN00181; EGF; S.
INTS; SN00181; EGF; S.
IN
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EMBL; AB011536; BAA32464.1; -.
HSSP; PO0740; IEDM.
Genew; HGNC:3230; CELSR3.
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                    1347 OPSSQAGFTCECQEGWMGPLCDQRTNDPC-LGNKCVH-GTCLPINAFSYSCKCLEGHGGV 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 AEPLALGRWHRVSAERLANKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVE----P 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 MPAGEYEFOCLCRDGFKGDLCEHEEN-PCQLREPCLHGGTCQ-----GTRCLCLPGFSGP 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 GPDATC----VNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPAL----T 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 HC----PTCRDRPCQNGGQCHDSESSYVCVCPAGFTGSRCEHSQAL-----HCHPEAC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 NTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLA-VLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor (Flamingo
factor-like domains 2)
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 3 precursor (Flamingo Monolog 1) (hFmil) (Multiple epidermal growth factor-like 1).
CELSR3 OR CDHF11 OR FMI1 OR EGFL1 OR MEGF2.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       N-LINKED (GLCNAC. . .) (POTENTIAL).
S -> SDEEE (In isoform 2).
/FIId=VSP 050035.
Missing (In isoform 2 and isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F11 = SOURNCE FROM N.A. MEDLINE-21202599; PubMed=10716726; MU Q., Maniatis T.; Wu Q., Maniatis T.; "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes."; Feature of protocadherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1529;
                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 397.5; DB 1; Length 29.7%; Pred. No. 1.6e-17; vative 58; Mismatches 141; Indels
                                                                                                                                                                                                                                        226 226 Q -> K (IN REF. 2).
607 610 SLM: -> KPQN (IN REF. 3).
634 634 L -> M (IN REF. 3).
1529 AA; 169869 MW; 5D19CC5E7FD461BA CRC64;
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TISSUE-Brain;
MEDLINE-99360089; PubMed-9693030;
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EGF-LIKE 7.
CALCIUM-BINDING.
EGF-LIKE 6.
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CALCIUM-BINDING.
EGF-LIKE 9.
EGF-LIK
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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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1895 IHVGGLPPG----SAESAPQGLVGCIQGVWLGSTPSGSPALLPP-----SHRVNAEPGCVV 1946
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                                                                                                                                                                                                                                                                                                                                                         283 SCGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEP--LALGRWHRVSAERLNK---
                                                                                                                                               ---GPIGCVRELR-----IQGEEIVFHDLNLTAHGISHCP------TCRDR
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                                                                                                                                                                                                                                                                                                                    -----DGSLRVNGGRPV-----LRSSPGKSQGLNLHTLL
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2474 2474 N-LINKED (GLCNAC. . .) (POTENTIAL)
2506 2506 N-LINKED (GLCNAC. . .) (POTENTIAL)
2158 2158 G -> GLRGAG (IN REF. 2).
3312 AA, 358251 MW, BEC208703651A4A5 CRC64;
                                                                                                   221;
                                                                    Query Match
Best Local Similarity 23.8%; Pred. No. 3.8e-17;
Matches 174; Conservative 83; Mismatches 252; Indels 221;
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1 EIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705
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Copyright (c) 1993 - 2004 Compugen Ltd.
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	Description .	O00468 homo sapien	Q8n7y0 homo sapien	Ospans mnscnln	Q9nfs9 drosophila			_	_	Q8irv8 drosophila		Q9v7i4 drosophila	Q9ngv2 drosophila	Q8nal2 homo sapien	Qabu56 mus musculu	Q9vqb1 drosophila	Q9u7e8 caenorhabdi
SUMMARIES	ΩI	000468	QBN7YO	Q8BGP3	Q9NFS9	Q9NEG1	Q8IRV9	Q9W4Y4	QBMPN3	QBIRV8	Q961C1	Q9V7I4	Q9NGV2	Q8NAL2	Q8BU56	Q9VQB1	Q9U7E8
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dР	Query Match	23.6	22.0	21.4	21.2	21.2	21.2	21.2	21.2	21.2	18.4	17.4	17.4	16.4	15.2	15.1	13.4
	Score	901.5	840	820	812.5	812.5	812.5	812.5	812.5	812.5	703	664.5	664.5	628	581.5	576.5	511
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479	464.5	420.5	419.5	412.5	412.5	411.5	407.5	407	407	402.5	402.5	394.5	393.5	390	387.5	387.5	387	385.5	385.5	385	380.5	377.5	375	370.5	367	363	362.5	361.5
17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	. 45

## AL IGNMENTS

	PRT; 2026 AA.		Creat	Last	25, Last annotation update)			Craniata; Vertebrata; E	Primates; Catarrhini; Hominidae; Homo.				<pre>Groffen A.J.A., Buskens C.A.F., Van Kuppevelt T.H.M.S.M.,</pre>	van den Heuvel	. (86		ъ.		ulos M., Soares M.B.;	"The I.M.A.G.E. Consortium: an integrated molecular analysis of	ion.";	•			r R., Gesemann M., Chiquet M., Ruegg M.A.;		1;				ral molecule activity; IEA.	Agrin_NtA.	BGF_like.			Laminin_EGF.	Laminin_G.
	PRELIMINARY;		_	_	(TrEMBLrel.	AGRIN precursor (Fragment).	B (Human).			9096;		OM N.A.	.A., Buskens	Veerkamp J.H., Monnens L.A.H.,	Eur. J. Biochem. 0:0-0(1998).		SEQUENCE OF 1-153 FROM N.A.	MEDLINE=96224170; PubMed=8617505;	Auffray C.,	G.E. Consort:	genomes and their expression.";	:151-152 (199		SEQUENCE OF 1-153 FROM N.A.	Dehzer A.J., Brandenberger	J. Cell Biol. 0:0-0(0).	EMBL; AF016903; AAC39776	U84406; AABS2917.1;	0; 1EDM.	:329; AGRN.	F: Btr					٠.	IPR001791; La
89	000468	000468;	01-JUL-1997	01-NOV-1998	01-OCT-2003	AGRIN precu	Homo sapiens (Human)	Eukaryota;	Mammalia, Butheria;	NCBI TaxID=9606;	[ <u>T</u> ]	SEQUENCE FROM N.A.	Groffen A.J	Veerkamp J.	Eur. J. Bio	[3]	SEQUENCE OF	MEDLINE=962	Lennon G.,	"The I.M.A.	genomes and	Genomics 33	[3]	SEQUENCE OF	Dehzer A.J.	J. Cell Bio	EMBL; AF016	EMBL; U8440	HSSP; P00740;	Genew; HGNC:329; AGRN	GO; GO:0005198;	InterPro; I	InterPro; I	InterPro; I			InterPro; I
000468	A	Ä	FQ.	Ιď	IO	DE	SO	ပွ	႘	ŏ	RN	RP	Z	æ	꿃	RN	RP	ă	æ	RT	RT	RL	RN	RP	æ	Æ	DR.	띥	g	H	E,	Ä	DR	JR	DR.	DR	D.R

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287 LVRATGTNRGFQGCVQSLAVNGRRI---DNRPWPLGKALSGADVGECSSGICDEASCIHG 343
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1886 LVLWS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLRVVAHRE 1941
                                    616 GRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLIGGRFSSGIIGCVKNL 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD-YG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 AIPKAGLSSGFIGCVRELRIQGEEIVFHDLM-----LIAAGISHCPT--CRDRPCQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BIKITERPDSADGMALYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
22.0%; Score 840; DB 4; Length 775;
Best Local Similarity 29.6%; Pred. No. 3.6e-54;
Matches 214; Conservative 107; Mismatches 257; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                    (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel, 25, Last annotation update)
                                                                                                                                                    2002 VVGR------HPLHLLEDAVTKPELRPCPT 2025
                                                                                                                 674 VLHSARPGAPPPOPLDLQHRAGAGANTRPCPS 705
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                                                                                                                                                                                                                                                                                  01-007-2002 (TrEMBLrel. 22, Cr
01-007-2002 (TrEMBLrel. 22, La.
01-007-2003 (TrEMBLrel. 25, La.
Hypothetical protein FLJ40230.
Homo sapiens (Human).
                                                                                                                                                                                                                                                     PRELIMINARY;
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OBN7Y0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1543 APCONLEAGRFHCOCPPGRVGPTCADEKS-PCOPNPCHGAAPCRVLPEG-GAQCECPLGR 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1377 LALBERALEPQGLLLYNGNA------RGKDFLALALLDGRVQLRFDTGSGPAVLT 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNBELYLGGYPD---Y 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GAIPKAGLSSGFIGCVRELRIQGEEIVFHDLNL-----TAHGISHC--PTCRDRPCQNG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 GOCHDSESSSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGR 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 KDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 NGKRL------DLTYSFLGSQGIGQCYDSSPCER---QPCQHGATCMPAGEYEFQC 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRPDAGSGMATIR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGLRCEEGVTVTTPSLSGAGSYLALPALTNTHHELR-------LDVBFKPLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1601 EGTFCQ-----TASGQDGSGPFLA-DFNGFSHLELRGLHTFARDLGEKMALEVVFLARGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1775 GGRQLLTPEHVLRQVDVT-SFAG-----HPCTRASGHPCLNGASCVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 LEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET-----IELEVRISTASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 23.6%; Score 901.5; DB 4; Length 2026; Best Local Similarity 32.2%; Pred. No. 3.2e-58; Matches 242; Conservative 93; Mismatches 266; Indels 151; Gaps
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2026 AA; 212881 MW; 4ABOEE710CD4B8EF CRC64;
                                                                                                                                                                        ERINTS PROOUL BEFLANING.

SWART; SMOO180; EGF Lam; 2.

SWART; SMOO274; FOLN; 5.

SWART; SMOO202; FAZAL; 9.

SWART; SMOO202; EAG; 1.

SWART; SMOO202; EGF 1, 6.

PROSITE; PSO1286; EGF 2; 1.

PROSITE; PSO1289; LAMININ TYPE EGF; 1.

PROSITE; PSO1249; LAMININ TYPE EGF; 1.
                                                                       ram; PP00050; kazal; 9.
Pfam; PP00053; laminin EGF; 2.
Pfam; PP03146; NRA; 1.
Pfam; PP01390; SEA; 1.
            InterPro; IPR000082; SEA domain.
InterPro; IPR008993; TIMP like.
InterPro; IPR001455; UPF0033.
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Q9NFS9
ID Q9NF
AC Q9NF
DT 01+0
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                                                                                                                                                                                                                                                                                                                                       DDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDG 581
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C STRAIN=2235463; TISSUB=Forelimb, Skin, Testis, and Thymus;

X MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

I "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDANs.";

IN Nature 420:563-573(2002).

IN RMBL; AK031135; BAC2875.1; -

R EMBL; AK031332; BAC2875.1; -

R EMBL; AK031233; BAC2875.1; -

R EMBL; AK03123; BAC2875.1; -

R MGD; MG1:2146149; AU04037.

R GO; GO:0005509; F:calcium ion binding; IEA.
                                                                                                                                                              DKOXIVEGMAEGGFTQIKCNTDIFIGGVPNYDDVKKNSGVLKPFSGSIQKIILMDRTIHV
                                                                                                                                                                                                                                                  GGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRV
                                                                                    TYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBGP3;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical EGF-like domain.
AUG40377.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO: GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR000742; EGF_Z.
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR008509; EGF_like.
InterPro; IPR003961; FN III subd.
InterPro; IPR008957; FN III.
InterPro; IPR00810; IEGF.
InterPro; IPR001791; Laminin_G.
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InterPro; IPR006210;
InterPro; IPR001791;
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ALYVGGMKEIALHTNRQYLRGLVGCISHFTLST-----DYHISLVEDAVDGRNINTC 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 GKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOCHDSESSSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 YSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYBFQCLCRDGFKGDLCEHBENPCQLR
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 BIKITERPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                                                                                                                                                         Length 1009;
Pfam; PF00041; fin3; 2.
Pfam; PF00054; laminin G; 3.
Pfam; PF00054; laminin G; 3.
PRINTS; PR00014; FWTVPEIII.
SMART; SM00109; EGF_CA; 2.
SMART; SM00060; FN3; 2.
SWART; SM0022; Lamd; 3.
PROSITE; PS00022; EGF_1; 3.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS00186; EGF_2; 2.
PROSITE; PS0025; LAMG_DOMAIN; 3.
Hypothetical protein.
SEQUENCE 1009 AA; 109834 MW; 80DD954F255C102B CRC64;
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Last sequence update)
                                                                                                                                                                                                                                                                                       Query Match
21.4%; Score 820; DB 11;
Best Local Similarity 29.3%; Pred. No. 1.6e-52;
Matches 211; Conservative 109; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NFS9 PRELIMINARY;
Q9NFS9;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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523 DGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGH
                                                                                                                          583 LVFRYQLGSGEARLVSED-PINDGEWHRVTALREGRRGSIQVDGEELVSGRS-PGPNVAV
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                                                                                                                                                                                                                                                                                                                      641 NAKGSVYIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANT
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Wirphy L., Harris D., Barrell B.;
"Sequencing the distal X chromosome of Drosophila melanogaster.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
EG:BACRASES 11 protein.
TROL OR EG:BACRASES 11 OR CG7981.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ALL138972; CAB72284.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PlyBase, Pegno001402; trol.

PlyBase, Pegno001402; trol.

GO; GO:0003676; F:mucleic acid binding; IEA.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF 2.
InterPro; IPR006210; EGF 1.
InterPro; IPR005109; EGF 1.
InterPro; IPR001701; IG-1ike.
InterPro; IPR001701; IG-1ike.
InterPro; IPR001701; IG-1ike.
InterPro; IPR001701; IDL_receptor_A.
InterPro; IPR001701; IDL_receptor_A.
InterPro; IPR000172; LDL_receptor_A.
InterPro; IPR000172; LDL_receptor_A.
Pfam; PP000047; ig; 2.
Pfam; PP000057; Idl_recept_a; 1.
Pfam; PP000057; Idl_recept_a; 1.
SWART; SM00181; EGF; 2.
SWART; SM00181; EGF; 2.
SWART; SM00182; LDLa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1035 AA
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PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS508035; LAM G DOMAIN; 3.
PROSITE; PS50065; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 1.
PROSITE; PS00030; RRM RNP 1; 1.
PGGF-1ike domain; Immunoglobulin domain.
SEQUENCE 1035 AA; 114044 MW; 413DE7EDI
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Q9NEG1;
01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 PTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNBELYLGGYPDYGAIP 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYTCICOPGWIGRDCA-IEGTOCTPGVCGA-GRCENTEN--DMECLCPLNRSGDRCQYNE 255
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                                                                                                                                                                                                                                                                                             Priedrich M.V.K., Schneider M., Timpl R., Baumgartner S.; "Perlecan domain V of Drosophila melanogaster: Sequence, recombinant analysis and tissue expression."; Submitteed (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ27462; CAB70094.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.2%; Score 812.5; DB 5; Length 708; larity 30.2%; Pred. No. 3.6e-52; Conservative 121; Mismatches 304; Indels 81;
                                                     Perlecan domain V (Fragment).
TROL OR EGIBARZESB3.11 OR CG7981.
Bukaryota; Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       708 AA; 77786 MW; 7B67C6F290642B98 CRC64;
                     01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flygase; PBgn0001402; trol.

GO; GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR000142; EGF 2.

InterPro; IPR006219; EGF 7.

InterPro; IPR006219; EGF 7.

InterPro; IPR001791; Laminin G.

InterPro; IPR001791; Laminin G.

InterPro; IPR00181; EGF; 3.

Pfam; PF00008; EGF; 3.

Pfam; PF00008; EGF; 2.

SWART; SW00181; EGF; 2.

SWART; SW00282; LamG; 3.
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PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00186; EGF_2; 3.
PROSITE; PS00030; LAM G DOWAIN; 3.
EGF-11ke domain.
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Matches 219; Conserv
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=7227;
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                                                      22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TVTTPSLSGAGSYLA---LPALTWTHHELRLDVEFKPLA-PDGVLLFSGGKSGPVEDFVS 295
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[1]
Length 1035;
                                                      Indels
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Last annotation update)
21.2%; Score 812.5; DB 5;
ilarity 30.2%; Pred. No. 6e-52;
Conservative 121; Mismatches 304;
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01-WAR-2003 (TrEWBLrel. 23, Created)
01-MAR-2003 (TrEWBLrel. 23, Last seq
01-OCT-2003 (TrEWBLrel. 25, Last ann
CG7981-PC.
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                           Best Local Similarity
Matches 219; Conserv
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Galle R.F.,
Adams M.D., Celliker S.E., Holf R.A., Gabler R.A., Galle R.F.,
Adams M.D., Lewis S.E., Richards S.A. Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
B. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
R.A. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
B. Ballew R.M., Basu A., Barendale J., Barankoch C., Baldwin D.,
B. Besson K.Y., Bence P.V., Berman B.P., Bhandari D., Brottier P.,
R.A. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R. Borkova D., Botchan M.E., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Bullon B.C., Dunn P.,
R.A. Charler M.L., Brong Z., Mays A.D., Dew I., Dietz S.M.,
R.A. Choup L.E., Downes M., Dugan-Rochas S., Dunkov B.C., Dunn P.,
R.A. Godek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harrish N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R.A. Harris N.L., Harvey D., Heiman T.J., Wein M.-H. Ibegwam C.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J. J., Li Z., Liang Y., Lin X.,
Allali M., Mallehla B., McIntesh T.C., Morris S., Kulp D., Lai Z.,
R.A. Markueil B., McIntesh T.C., Morris J., Moshrefi A.,
R.A. Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
R.A. Mount S.M., Moy M., Murphy D., Murphy L., Murphy D.M., Nelson D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGKSQGINLHTILIYLGGVEPS-VPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQG 412
                                                                                                                                                                                                 3841 IQSC------GETNMIGGDEDSDNEPPVPPPTPDVHENELQPYAMAPC-ASDP
                                                                                                                                                                                                                                                                 467 CLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHD
                                                                                                                                                                                                                                                                                                                                     3887 CENGGSCSEQEDVAVCSCPFGFSGXHCQE-----HLQLG------PNASFRG
                                                                                                                                                                                                                                                                                                                                                                                                      DGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 LVFRYQLGSGEARLVSED-PINDGEWHRVTALREGRRGSIQVDGEELVSGRS-PGPNVAV
                                                                                                                                    413 IGQCYDSSPCERQPCQHGATCMPAGEYE-----FQCLCRDGFKGDLCEHEENPCQLREP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CG7981 protein.
TROL OR ECIBARREB3.11 OR CG7981.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroida; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3439 ELTFRPENGDGLLLFNGOTRGSG------DYIALSLKDRYAEFRFDFGGKFMLVRA 3488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 KAGLSS--GFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSES-S 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVTTPSLSGAGSYLA---LPALTNTHHELRLDVEFKPLA-PDGVLLFSGGKSGPVEDFVS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAMVGGHLEFRYELGSGL--AVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 SYVCYCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KITPRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIRH
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Local Similarity 30.2%; Score 812.5; DB 5; Length 4;
Local Similarity 30.2%; Pred. No. 3.9e-51;
(e8 219; Conservative 121; Mismatches 304; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RNP 1; 1.
454841 MW; BB47056B7B4D6106 CRC64;
                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003424; AAN09077.1; -.
                                                                                                    EMBL; ABLOUSER; ASSOCIATION, TEPBRES, FBERNOOU1402; LTO., GO, GO:0003677; F:DNA binding; IEA.
GO, GO:0003198; F:STRUCTURAL MOLECULE activity; IEA.
GO, GO:00063108; F:STRUCTURAL MOLECULE activity; IEA.
INTERPRO; IPRO10525; C5_DNA meth.
INTERPRO; IPRO10958; ConA like_lec_gl.
INTERPRO; IPRO105209; EGF 2.
INTERPRO; IPRO105209; EGF 1.
INTERPRO; IPRO105209; EGF 1.
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EGF 1; 10.
EGF 2; 6.
IG LIKE; 11.
IAMININ TYPE EGF; 7
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InterPro; IPR000504; RNA_rec_mot.
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Pfam; PF00052; laminin B; 3.
Pfam; PF00053; laminin EGF; 2.
Pfam; PF00054; laminin G; 3.
Pfam; PF00057; ldl recept a; 23.
PRINTS; PR00261; LDLREGEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laminin_EG
Laminin_G.
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Laminin_B.
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SWART; SW00180; EGF Lam; 6.
SWART; SW00409; IG; 12.
SWART; SW00409; IGC2; 12.
SWART; SW00281; LamB; 3.
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InterPro;
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3783 LVLRGGHABLLINTAARLDPVVVRSAEPLPLNRWTRIBIRRRLGEGILRVGDGPERKAKA 3842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3949 CENGGSCSEQEDVAVCSCPFGFSGRHCQE------HLQLG------FNASFRG 3989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3671 AYTCICQPGWTGRDCA-IEGTQCTPGVCGA-GRCENTEN--DMECLCPLANKSGDRCQYNE 3726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGH 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 PGKSQGINIHTILYLGGVEPS-VPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQG 412
                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 NAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 CLHGGTCOGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHD
                                                                                                                                                                                                                                                                                                                                                                                                       3501 ELTERPENGDGLLIENGQTRGSG------DYIALSLKDRYAEFREDFGGKPMLVRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 PTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEBLYLGGYPDYGAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 KAGLSS--GFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSES-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 SYVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYICRCHLGRSGLRCEEGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 IGOCYDSSPCEROPCOHGATCMPAGEYE-----FOCLCRDGFKGDLCEHEENPCOLREP
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                                                                                                                                                                                                                                                                                                                                                                               3 KITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPBFRFDAGSGWATIRH
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                             Length 4179;
R SMART; SM00180; EGF Lam; 9.

R SMART; SM00409; IG; 12.

R SMART; SM00281; JamB; 3.

R SMART; SM00282; LamB; 3.

R SMART; SM00282; LamB; 3.

R SMART; SM00192; LDLR, 3.

R SMART; SM00192; LDLR, 1.

R PROSITE; PS00094; C5 MTASE 1; 1.

R PROSITE; PS01186; EGF 1; 10.

R PROSITE; PS01186; EGF 1; 10.

R PROSITE; PS01289; LAMININI TYPE EGF; 7.

R PROSITE; PS01209; LDLRA, 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.

R PROSITE; PS00030; RRM RNP 1; 20.
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                             Query Match
21.2%; Score 812.5; DB 5;
Best Local Similarity 30.2%; Pred. No. 4e-51;
Matches 219; Conservative 121; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1162 NVCPA 4166
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SEQUENCE
RESIDENCE FROM N.A.

REDLINES-20196006; PubMed=10731132;

Adame M.D., Celniker S.E., Holt R.A., Evans C.A., Gocgyne J.D.,

Adame M.D., Celniker S.E., Holt R.A., Evans C.A., Gocgyne J.D.,

Adame M.D., Celniker S.E., Holt R.A., Exhans C.A., Galle R.F.,

Amanatides F.G., Scherer S.E., Lip.M., Exhans C.A., Galle R.F.,

Button G.G., Wortman J.R., Plazel R.G., Champe M., Pfeitfer B.D.,

Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeitfer B.D.,

R. Brandon R.C., Barter E.G., Helt G., Nelson C.R., Gabor G.L.,

R.A. Abril J.F., Agbayani A., An H.J., Andrews-Farmkoch C., Baldbor B.D.,

R. Beson K.Y., Benos P.V., Bernal B.P., Bardatin D., Bolahakov S.,

R. Beson K.Y., Benos P.V., Bernal B.P., Bandatin D., Bolahakov S.,

R. Beson K.J., Canles D.A., Buller H., Cadieu E., Center A., Chandra I.,

R. Burtis K.C. Busam D.A., Bullke C., Davenpour L.B., Davies P.,

B. Durbin K.J., Evangeliste C., Ferraz C., Perriera S., Plaiser R.,

R. Doson K., Doup L.E., Downes M., Digan P., Brottler P.,

R. Doson K., Doup L.E., Downes M., Digan P., Rerista S., Fleischmann W.,

R. Follock A., Gong F. Gorrell J.H., Gu Z., Galbart W.H., Ibeywam C.,

R. Houst D.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

R. Houst M., Mallah R., Kalueh F., Karpen G.H., Ke Z., Kall P.D., Lai Z.,

Alalai M., Kalueh F., Karpen G.H., Ke Z., Kall P.D., Lai Z.,

Liu X., Mattei S., Molitceh T.C., Moraty C., Mornis J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,

R. Reinert K., Remington K., Saunders R., Vente B., Santh H.,

R. Spier B., Spietner S., Panner R., Vente E., Wang A.H., Wang X.,

R. Spier B., Stadier Kiamos I. Singson M., Stupski M., Stupski M.,

R. Sheng X.H., Zhong F.N., Weilsenbadh J.,

R. Sheng X.H., Wooder F.N., Weilsenbadh J.,

R. Sheng X.H., Woodes F.N., Weilsenbadh J.,

R. Sheng X.H., Zhong S., Zhong S., Zho O., Zhon J.,

R. 
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Barason J., An H., Balan D., Barason J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Agarg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
                                                                                                                                                                                                                                                                                                     "Perlecan participates in proliferation activation of quiescent Drosophila neuroblasts."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Perlecan (CG7981-PD).
TROL OR EG:BACR25B3.11 OR CG7981.
Drosophila melanogaster (Fruit fly).
Bukaryota, metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota, Bidopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                  QBMPN3
                                  RESULT 8
Q8MPN3
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McIncoch T.C., Wey M., Whypy B., Steinen C., Mellon K.A., Numoo J., Baclabo W.P., Baclabo W., Park S., Patell S., Petell S., Sanch H. V., Reiners S., Scheeler F., Stephenon W., Strong R., Strikes R., Tector C., Takbin G.M., Stephenon M., Strong R., Strikes R., Tector C., C., Rubin G.M., Stephenon M., Strong R., Strikes R., Tector C., C., Rubin G.M., M. Millans S., Caroby M.A., Martiese B. Bayrakaroglu L., Campbell K., M. Hirds S., Caroby M.A., Martiese B. B. Bayrakaroglu L., Campbell K., Misse S., Martiese B. B., Petell S., Ganth M., Cellinker S. E., Carlson J.M., Cellinker S. E., Anna S., Carlson J.M., Cellinker S. E., Santh B., Milland G., Richert J., Anna S., S., Martiese B. M., Cellinker S., E., Sha K., Daniel B., Milland G., Richert J., Anna S., S., Martiese B., Martiese B., de Grey A., Barris N., Santh B., Martiese B., Martiese B., Grown M., Cellinker S., E., Sha K., Daniel G., Martiese S., Carlson J.M., Cellinker S., E., Sha K., Daniel G., Marties S., Carlson J., Martiese B., Marties
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22;

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3655 ADAVSQQVGFVGCISRLTLQGRTVELIREAKYKEGITDCRPCAQGPCQNKGVCLESQTEQ 3714
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                                                       3545 ELTERPENGDGLLLENGQTRGSG------DYIALSLKDRYAEFREDFGGKFMLVRA 3594
                                                                                                                                                                                                              3595 EEPLALNEWHIVRVSRFKRDGYIQVDEQHPVAFPTLQQIPQLDLIEDLYIGGVPNWELLP 3654
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                                                                                                                                                      63 PTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGAIP 122
                                                                                                                                                                                                                                                                                                                 123 KAGLSS--GFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSES-S 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SYVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGV 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMVGGHLEFRYELGSGL -- AVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 PGKSQGLNLHTLLYLGGVEPS-VPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 CLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHD 522
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3 KITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIRH 62
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RESULT 9
QBIRVB
ID QBIRVB
AC QBIRVB
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT CG7981-PE.
GT981-PE.
GT981-PE.
GT981-PE.
GT981-PE.
GN TRCL OR EGABACKSEB3.11 OR GG7981.
OC EUKATYOCIA Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea, Drosophila metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea, Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gocayne J.D., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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Buller G.G., Wortman J.R., Vandell N.D., Zhang Q., Chen L.X., D. R. Buller R. M., Beat A., Bardello M.D., Cland G., Naprathracid C., Impedent C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Estimate C., Es
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4157
                                                                                                                                                                                      3998 CENGGSCSEQEDVAVCSCPFGFSCKHCOE-----HLOLG-----FNASFRG 4038
                                                                                                                                                                                                                                                                                                 227 HIGRSGLRCEEGVTVTTPSLSGAGSYLALPALINTHHELR------LDVEFK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 PLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 583 LVFRYQLGSGEARLVSED-PINDGEWHRVTALREGRRGSIQVDGEELVSGRS-PGPNVAV 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 NAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPOPLDLOHRAQAGANT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CHGGAPCQNLEAGRFHCQCPPGRVGPTCADEKS-PCQPNPCHGAAPCRVLPEG-GAQCEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 PLGREGIFCO----TASGODGSGPFLA-DFNGFSHLELRGLHTFARDLGERMALEVVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 CONGGOCHDSESSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRC
413 IGQCYDSSPCERQPCQHGATCMPAGEYE-----FQCLCRDGFKGDLCEHEENPCQLREP
                                                   3952 IQSC------GETNMIGGDEDSDNEPPVPPPTPDVHENELQPYAMAPC-ASDP
                                                                                                                                                                                                                                                        523 DGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                467 CLHGGTCQGTR----CLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 703; DB 4; Length 488; 33.2%; Pred. No. 3.4e-44; ive 63; Mismatches 196; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Straubberg R.;
Straubberg R.;
Straubberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR006985; ConA like.lec_gl.
InterPro; IPR006209; EGF like.
InterPro; IPR006109; EGF like.
InterPro; IPR0061791; Laminin_G.
Pfam; PF00008; EGF; 3.
Pfam; PF00008; EGF; 3.
Pfam; PF00054; laminin_G; 2.
SWART; SW00181; EGF; 2.
PROSITE; PS00022; LamG; 2.
PROSITE; PS00022; LaM G DOWAIN; 2.
PROSITE; PS0025; LAM G DOWAIN; 2.
PROSITE; PS0025; LAM G DOWAIN; 2.
NOW TER
SEQÜENCE 488 AA; 51764 MW; A732B99CC680E772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.24
Matches 191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4211 NVCPA 4215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      701 RPCPS 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96IC1
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Q96IC1 ,
ID Q96IC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3660 ADAVSQQVGFVGCISRLTLQGRTVELIREAKYKEGİTDCRPCAQGPCQNKGVCLESQTEQ 3719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3720 AYTCICOPGWIGRDCA-IEGTOCTPGVCGA-GRČENTEN--DMECLĆPLNRSGDRCQYNE 3775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3832 LVLRGGHAELLINTAARLDPVVVRSARPLPLNRWTRIEIRRRLGEGILRVGDGPERKAKA 3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || : |:| | ||:| | : | | :: | |:: | ||: | PGSDRILSLKTHLYVGGYDRSTVKVNRDVNITKGFDGCISRLYNFQKPVNLLADIKDAAN 3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3550 ELTFRPENGDGLLLFNGQTRGSG------DYIALSLKDRYAEFRFDFGKPMLVRA 3599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 KAGLSS--GFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSES-S 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYICRCHLGRSGLRCEEGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 TVTTPSLSGAGSYLA---LPALTNTHHELRLDVEFKPLA-PDGVLLFSGGKSGPVEDFVS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAMVGGHLEFRYELGSGL--AVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGKSQGLNLHTLLYLGGVEPS-VPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 PTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%; Score 812.5; DB 5; Length 4228; 30.2%; Pred. No. 4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRM RÑP 1; 1.
.; 466934 MW; 0F630AA0BBF4CD33 CRC64;
                                                   P. Brructural molecule activity; IEA P. DNA methylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG LIKE; 11.
PROSITE; PS501248; LAMININ TYPE EGF; 7.
PROSITE; PS50025; LAM G DOMAIN; 3.
PROSITE; PS50068; LDLRA 1; 21.
PROSITE; PS50068; LDLRA 2; 24.
                                                                                                                                                                                                                                                                         InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR0001398; Ig.c2.
InterPro; IPR002049; Laminin_Br.
InterPro; IPR002049; Laminin_Br.
InterPro; IPR00172; Lot. receptor_A.
InterPro; IPR002172; Lot. receptor_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PP00047; ig; i2.
Pfam; PP00052; laminin B; 3.
Pfam; PP00054; laminin GGF; 2.
Pfam; PP00054; laminin G; 3.
Pfam; PP00057; ldl recept a; 24.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laminin_B; 3
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EXCURANCE FROM N.A.

REATIN=BERKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Holt G., Change M., Henderson S.N.,

RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Change M., Petiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Baldwin D.,

RA Ballew R.M., Bouck J., Brokestein P., Brottler P.,

RA Berkova D., Botchan M.R., Bouck J., Brokestein P., Brottler P.,

RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K.J. Bownes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fesischmann W.,

RA Roeler C., Gabriellan A.E., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris M., Kallush F., Karpen G.H., Re Z., Kennison J.A.,

RA Jalai M., Kallush F., Karpen G.H., Re Z., Kennison J.A.,

RA Liu X., Mattei B., McIntosh T.C., McLedd M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mobarry C., Morris J., Noshrefi A.,

RA Mount S.M., Mount S.M., Murphy L., Murry D., M., Noshrefi A.,

RA Mount S.M., Moy M., Murphy L., Murry D., M., Noshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murry D., M., Noshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,

RA Merkulov G., Moy M., Murphy L., Murry D., March S. M. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        669
                                                                                                                                                                                                                                                                                                                                                    344 ATOGLVLWS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLRVV 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459
                                    551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VEKSAG-------DVDTLAPDGRTFVEYLNAVTESEKALQSNHFELSLRTE 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 TASGLLLWQGVEVGEAGQGKOFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVT 611
ERLINKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVG 392
                                                                                                                                                    EVSVNGKRL------DLTYSFLGSQGIGQCYDSSPCER---QPCQHGATCMPAGEY 439
                                                                                                                                                                                                                                                                                                    440 EFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIAE 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 SDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET------IBLEVRTS
                                                                                                                                                                                            612 ALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLIGGRFSSGITGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG8403 protein.
SP2353 OR CG8403.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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A grane C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Branzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A dodon K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Houland T.J.,
Ibeyam C., Jalail M., Kruse D., Li P., Mattei B., Moshrefi A.,
A millane C.W., Park S., Patel S., Pfeiffer B.,
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"Sequencing of Drosophila melanogaster genome.";
Supmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Skeinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Syradling A.C., Fapleton M., Skupski M.P., Smith T., Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wang S.-Y., Wassaraman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Warley K.C., Mu. D., Yang S., Yao Q.A., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng R.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu X., Smith H.O., The genome sequence of Drosophila melanogaster.";
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Mistage S., Croeby M.A., Matthews B.B., Bayraktaroglu L., Campbell K
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale K., Emmert D., Frise E., de Grey A., Harris N.,
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Pred. No. 1e-40;
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SMART; SM00181; EGF; 4.
SMART; SM00181; EGF; 4.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01025; LAM_G.DOMAIN; 3.
EGG-1ike domain.
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EMBL; AE003808; AAF58071.2;
HSSP; P08709; 1BF9.
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                    VLTISSNGFWHLSLDQNLFVGGVNHVDRLPLDLKYKPFFVGCIQRIDINGHSLGIVAEAL
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                                             Alpkaglssgfigcvrelriggeeivfhdlnltah------Gishcpt--crdrpcq
                                                              LAKRIPLAEGFAGCIR--RFVANE---HDYKRTEHPLGDVINGFDIQDCSTDKCVRYPCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AIPKAGLSSGFIGGVRELRIQGEEIVFHDLNLTAH-----GISHCPT--CRDRPCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGGQCHDSESSSYVCVCPAGFTGSRCEHSQALHCHPRACGPDATCVNRPDGRGYTCRCHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIRSSPGKSQGLNIHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 BIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 QLRIEFRPESFDGIILLSGER------DDLTGDFWALLINKGFVEFWFDCGSGVGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1361;
       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Metocoa; Moptera; Brachycera; Muscomorpha; Ebhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                               SEQUENCE FROM N.A.
Serano T.L., Pendleton J.D., Rubin G.M.;
A reverse genetic screen for genes involved in Drosophila development.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1361 AA; 150355 MW; 206D9F9BF9EDFE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.4%; Score 664.5; DB 5;
Best Local Similarity 22.0%; Pred. No. 1e-40;
Matches 221; Conservative 111; Mismatches 295;
                                                                                                                                                                                                                                                                                                                                 FlyBase; FBD00344070; SP2353.
InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR006209; BGF Ilke.
InterPro; IPR006210; IBGF.
InterPro; IPR001791; Laminin_G.
Pfam; PP00008; BGF; 1.
Pfam; PP0054; laminin_G; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGGKCLPSDQGA-ICLCPIGFVGDLCE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS50025; LAM G DOMAIN; 3.
                                                                                                                                                                                                                                                                                            EMBL; AF239610; AAF63502.1;
HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 PCLHGGTCQGTR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00181; EGF; 3.
SMART; SM00282; LamG; 3.
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EGF-like domain.
SEQUENCE 1361
OR CG8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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LTAHGISHCPT--CRDRPCQNGGQCHDSESSYVCVCPAGFTGSRCEHSQALHCHPEACG 208
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical EGF-like domain.
                 680 PGAPPPOPLDLOHRAQAGANTRPC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 -----DYHISLVEDAVDGKNINTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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A Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

A Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

A Creul, T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y.,

A Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagateuma M.,

A Murakawa K., Kanehori K., Takahashi-Fujil A., Oshima A., Suzuki Y.,

A Wurakawa K., Magahari K., Masuho Y., Nagal K., Isogai T.;

A Sugano S., Nagahari K., Masuho Y., Nagal K., Isogai T.;

Exabo human cDNA sequencing project.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

B Shal, AXO92479; BAC03900.1;

C GO:0005509; Frcalcium ion binding; IEA.

B InterPro; IPR001881; EGF Zike.

B InterPro; IPR001891; EGF Zike.

B InterPro; IPR001791; Laminin G.

B Ffam; PP00008; EGF; Z.

B Ffam; PP00008; EGF; Z.

B Ffam; PP00008; EGF; Z.
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                                                                                                                                                                                                                                                                                                                     .080 MKRIMSNSNAHSSHKKAEVQFPPQGSQEVGTANEDTSQYSDDYNDDELLTPVWQGGEEVK 1139
                                                                                                                                                                                                            1140 LEQHTSSTPQTHTDWSLLKKFDLSAEHQSQVQGVRKNPGACFAGSDSYFHYNDADTMSQV 1199
                                 960 PRLSGKHHASKHEHHLKPNAAFTRKLSRLPTHYESFQTNPDSDILTFEDNNDWVTSLQQQ 1019
                                                                                                                                                                                                                                           592
                                                                                                                                                                                                                                                                                                    593 EARL-VSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGA 651
                                                                                        1020 EYGDAMAASQVPLAFEDASPGTPRSSDNNEDDENAFVFDESLFDASDGTEEYQRKQLAQD
                                                                                                                                                                                                                                           533 FSRSLPEVPETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSG
                                                                                                                                                                                                                                                                       1200 ISYSI-----DINLRIKTHSENGVILWTGRQ-GTTEEHDDYLSLGIEQGYLHFRYDLGSG
                                                                                                                       493 -----SGHGIAESDWHLEGS----GGNDAPGQYGAYFHDDGFL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
16.4%; Score 628; DB 4; Length 463;
Best Local Similarity 28.7%; Pred. No. 1.3e-38;
Matches 162; Conservative 80; Mismatches 198; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                   652 PDVATLIGGRESSGIIGCVKNLVLHSARPGAPPPQPLDLOHRAQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00181; EGF; 2.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF (24, 2.)
SMART; SM001282; LamG; 2.
PROSITE; PS00122; EGF 1; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01055; LAM G DOMAIN; 2.
HYPOCHELICAL DECLEIN; EGF-11ke domain.
SEQUENCE 463 AA; 50635 MW; F688BF2714D5D0EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ35160.
Homo sapiens (Human).
                                                               ----PRCQQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
      482 PGFSG-
                                                               487 ----
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442 OCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGT--RCLCLPGFSGPRCQQGSGHGIAE 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            321
                                                                                                                        322 LALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGINLHTLLYLGGVEPSVPLSPAT 381
                                                                                                                                          520 SIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSAR
                           382 NMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSSPCEROPCOHGATCMPAGEYEF
                                                           -RLDVEFKPLAPDGVLLFS---GGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEP
                                                                            89 MEFEITFRPDSGDGVLLYSYDTGSK----DFLSINLAGGHVEFRFDCGSGTGVLRSEDP
                                                                                                                                                                                                                                                                                261 DCDCPLGFEG------LH---CQKAIIEAIEIPQFIG------
                                                                                                                                                                                                                                                                                                                500 SDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLW
                                                                                                                                                                                                                                                                                                                                                                              560 QGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRG
209 PDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSL-SGAGSYLALPALTNTHHEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKETYCTE: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worman J.R., Yandell M.D., Zhang O., Chen L.X.,
Branch R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brancon R.C., Baxeer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A. An H.-J., Andrews Fennkoch C., Baldwin D.
RA Ballew R.M., Basu A., Baxendale J., Blandari D., Baldwin D.
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Broktein P., Brottae F.,
Burtis K.C., Busam D.A., Dahler H., Cadicu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Dahler H., Cadicu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Dahler H., Cadicu E., Center A., Chandra I.,
Burtis K.D., Evangelista C.C., Ferriac S., Dunkov B.C., Dunn P.,
RA Gebra C., Gabriellan A.B., Garra C., Ferriac S., Dunkov B.C., Dunn R.,
B. Durbin K.J., Farngelista C.C., Ferriac S., Dunkov B.C., Dunn R.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalaih M., Kalpen G.H., Re Z., Kanigon J.A., Etchman R.A.
Lasko P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
Rimmel B.E., Kodira C.D., Karft C., McLaod M.P., Morbleson D.L.,
Rakmel B.E., Kodira C.D., Warft C., Morris J., Moshrein R.,
Rainch W., Pittman G.S., Pan S., Pollard J., Moshrein R.,
Rainch W., Wilshin N.V., Mobarry C., Morris J., Moshrein R.,
Rainch W., Nelson K., Sandsen R., Pollard J., Morris R., Spier E., Spradling A.C., Staplecon M., Strong R., Suith H.,
Rang Z.-Y., Wassaman D.A., Weinsch M., Strong K., Shien H.,
Rang Z.-Y., Wassaman D.A., Ringcock G.M., Weissenbach J.,
Rang Z.-Y., Wassaman D.A., Ruing G., Zhao Q., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Siden-Kiamos I., Sulpsoon W., Zhao G., Zhao G., Zhao G., Zhao G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:1216-1219-1009.

EMBL, AR003583; AAF51266.1; -
HSSP; P00740; IEDM.

Flyaase: F8gr0031416; CG7245.

GO; GO:00331416; CG7245.

GO; GO:003676; F:nucleic acid binding; IEA.

InterPro; IPR000742; EGF?

InterPro; IPR001791; Laminin_G.

InterPro; IPR001791; Laminin_G.

InterPro; IPR001791; Laminin_G.

InterPro; IPR001791; Laminin_G.

Ffam; PF00008; EGF; 5.

Pfam; PF00008; EGF; 5.

Pfam; PF00008; EGF; 5.

PRAKT; SM0181; EGF; 6.

PROSTIE; PS01186; EGF; 7.

PROSTIE; PS01186; EGF 2; 3.

PROSTIE; PS01186; EGF 2; 3.

PROSTIE; PS01030; RRM_RNP_1; 1.

EGF-1ke domain.

SEQUENCE 1039 AA; 114305 MW; 8864EC2A0F3455
                    555
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                                                                                                                                                                                                                                                                                                                                                                                                               200 IHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPALT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 EPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGLN1HTLLYLGGVEPSVPLSP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 IXADSYICLCPLGFRG---RH--------CEDAFALTIPQF------RESLR 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                       403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATNMSAHFRGCVGEVSVNGKRLDLTYSFLG----SQGIGQCYDSSPCERQPCQHGATCMP 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASG
                                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                  Ouery Match
15.2%; Score 581.5; DB 11; Length 822;
Best Local Similarity 30.3%; Pred. No. 8.7e-35;
Matches 139; Conservative 70; Mismatches 184; Indels 65;
                                                                                                                                                                                                                                                                                                89669 MW; 225A01D56D8DE691 CRC64;
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Pfam; PF00008; EGF; 1.
Pfam; PF00004; fn3: 2.
Pfam; PF00004; fn3: 2.
PRINTS; PR0014; FNYYPEIII.
SWART; SW00181; EGF; 2.
SWART; SW00179; EGF CA; 1.
SWART; SW00060; FN3; 2.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                l protein.
822 AA; 8
                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 82
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                                                                                                                                                                                                                                TECGSLACLSSPCRNGAACIKIETNDLDENGEKAEKWKCKCPTGYMGPTCEISV---CED
                                                                                      70 HFHTVTL--LRSLT--QGSLIVGDLAPVNGTSQGKFQGLD------LNEELXLGGYP
                                                                                                         117 D--YGAI---PKAGLSSGFIGCVRELRIOG------BEIVFHDLN----LTAHGI
                                                                                                                                                                    Gaps
                                                          Indels 143;
                          Query Match
Best Local Similarity 27:2%; Pred. No. 2.8e-34;
Matches 200; Conservative 95; Mismatches 298; Indels 143;
1039 AA; 114305 MW; 8864EC2A0F345590 CRC64;
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SEQUENCE FROM N.A.
STRAIN=Berkeley;
BEDLINE-20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Bachyeera; Brachyeera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

RESULT 15
COYORI
1D COYORI
AC COYORI
DT 01-MA
DT 01-MA
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Q9VQB1; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) CG7245 protein.

PRELIMINARY;

Q9VQB1

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519 YFHDDGFLAFP-----GHVFSRSLPEVPET--------IBLE 547
                                                                                                                                                                                                                                                                                                                                                   526 YRNFTKKLMPPKPITTPSSHFVMKLLNBVEKQRSFSPVPLMGSKSFEEHHRVQFFFIEFQ 585
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                                                                                                                                                              372 E-----PSVPLSPATNMSAHFRGCVGEVSVNGKR----LDLTYSFLGSQGIGQCYDS 419
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                                                                                                                                                                                                                                   GTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGS------GGNDAPG----QYGA 518
                  179 NPCQYGGTCVQFP-GSGYLCLCPLGKHGHYCEHNLEVALESFSGSVNGLSSFVAYTVPIP 237
                                                     261 THHELRIDVEFKP--LAPDGVILFSG--GKSGPVEDFVSLAMVGGHLEFRYELGSGLAVI 316
                                                                       298 FIQKPIDFRLDAPRVPYEIKVGRIGRQAMLSVDGKFNITGRSPGSGSRMDVLPILYLGGH 357
205 BACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGA----GSYLALPALIN 260
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OM protein - protein search, using sw model

March 9, 2004, 17:19:48; Search time 85.8465 Seconds (without alignments) 2320.373 Million cell updates/sec Run on:

US-10-006-011A-3

Title: Perfect score:

1 BIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705 Sequence:

Scoring table:

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1586107 seqs, 282547505 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		o <del>k</del>			SUMMERIES	
Result No.	Score		Length	DB	ΩI	cript
Н	705	100.0	4391	9	AAE34390	Aae34390 Human per
7	443	62.8	4393	4	AAB31889	1889 Amino
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### ALIGNMENTS

AAE34390 standard; protein; 4391 AA.

(first entry) 14-MAY-2003

Human perlecan protein.

Human; diagnosis; ostecarthritis; rheumatoid arthritis; perlecan.

Homo sapiens.

WO200295415-A2.

28-NOV-2002.

22-MAY-2002; 2002WO-EP005612.

23-MAY-2001; 2001GB-00012626.

Christgau S, Henriksen DB, Cloos PAC; (OSTE-) OSTEOMETER BIO TECH AS.

WPI; 2003-140389/13.

An assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis comprising detecting an isomerized or optically inverted protein in a sample. 

Disclosure; Page 46-67; 106pp; English.

The invention relates to an assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The assay involves measuring (in a biological sample) the amount or presence of an isomerised or optically inverted protein or one or more isomerised or optically inverted fragments from proteins such as perlecan, biglycan, decorni, fibrillin-1 or protocadherin. The assay is useful for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The present sequence is human perlecan protein

Sequence 4391 AA;

Gaps ć o Query Match
100.0%; Score 705; DB 6; Length 4391;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 705; Conservative 0; Mismatches 0; Indels 0;

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EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI 3746
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The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymorleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the genglioside GMZ activator, calgranulin B or saposin B protein familias. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, proprection and treatment of multiple sclerosis (in its various forms and parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid playarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells

Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.

Claim 1; Page 138-152; 209pp; French.

Perron H;

Malcus C, Santoro L,

Charles M,

Roecklin D, Kolbe H, WPI; 2001-159475/16.

99FR-00009372.

15-JUL-1999;

(INMR ) BIOMERIEUX STELHYS.

Human, perlecan, retinol-binding plasma protein; calgranulin B; vaccine, ganglioside GNZ activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinoon's disease; amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy. Amino acid sequence of a human protein. AAB31889 standard; protein; 4393 AA (first entry) 15-MAY-2001 AAB31889; AAB3188 

17-JUL-2000; 2000WO-FR002057.

WO200105422-A2 Homo sapiens

3868 3928 ö 3749 RHPTPLALGHFHTVTLLESLTQGSLIVGDLAPVNGTSQGKFQGLDLNELYLGGYPDYGA 3808 3929 VTTPSLSGAGSYLALPALTWTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAAWG 3988 GHLEFRYELGSGLAVIRTAEPLALGRWHRVSAERLNYDGSLRVNGGRPVIRSSPGKSQGL 4048 4108 4169 LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPBV 4228 180 240 480 61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA 120 420 241 VTTPSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVG 300 481 LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV 540 9 3809 IPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESS 3689 RIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI 181 YVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVT 1869 YVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVT 1 BIKITFRPDSADGMLLYNGOKRVPGSPTNLANROPDFISFGLVGGRPEFRFDAGSGMATI 121 IPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESSS 301 GHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGL 361 NLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSS 4049 NIHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSS PCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLC 0; Gaps DB 4; Length 4393; 2; Indels 62.8%; Score 443; DB 99.7%; Pred. No. 0; Live 0; Mismatches Best Local Similarity 99.73 Matches 643, Conservative Sequence 4393 AA; 421 3989 Query Match 엄 ઠે 셤 셤 g 셤 ď ઠે g ઠે ઠે ઠે ઠ ઠે

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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                           4142 PCERQPCQHGATCMPAGEYEPQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV
                                                                                                                                                                                                                                 301 GHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGL
                                                                                                                                                                                                                                                                                                                                                                                                                    4202 LÞGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV
                                                                                                                                                  121 IPKAGLSSGFIGCVRELRIQGEBIVFHDLMLTAHGISHCPTCRDRPCQNGGQCHDSBSSS
                                                                                                                                                                                                                                                                        241 VTTPSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVG
                                                                                                                                                                                                                                                                                                                                                                                              NLHTILLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTXSFLGSQGIGQCYDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 PCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLC
                                                                                                              3842 IPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESSS
                                                                                                                                                                                                            181 YVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVT
                                                                                                                                                                                                                                                                                                                                                              4022 GHLEFRYELGSGLAVLRTAEPLALGRWHRVSAERLNXDGSLRVNGGRPVLRSSPGKSQGL
                                                   1 BIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                         61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA
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   Indels
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    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB31890 standard; protein; 195
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      583; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200105422-A2
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The present sequence represents a human polypeptide, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymorlectide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the retinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polymorlectides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid polyarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of pocential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 DAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPETIBLEVRTSTASGLLLWQGVEVGEAGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQG
                                      Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular Dementia; VD; VD-associated protein isoform; VPI; screening; diagnosis; prognosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                            27.7%; Score 195; DB 4; Length 195; 100.0%; Pred. No. 5.3e-183; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vascular dementia-associated protein isoform (VPI) 111.
                                                                                                     Claim 1; Page 152-153; 209pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB55911 standard; peptide; 18 AA.
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24-NOV-2000; 2000GB-00028734.
26-NOV-2000; 2000US-00724391.
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Matches 195; Conservative
 WPI; 2001-159475/16.
N-PSDB; AAF54728.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 195 AA;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for
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                                                                                                                                                                                                                                   Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                Rohlff C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 32; 151pp; English.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                          Herath HMAC, Parekh RB,
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Vascular dementia-associated protein isoform (VPI) 105.
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            Claim 6; Page 32; 151pp; English.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                                                                                                                                                                                                                   14-MAR-2001; 2001WO-GB001106.
                                                                                                                                                                   596 LVSEDPINDGEWHR 609
features correlated with VD
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-557937/62.
                                                                                                                                               Local Similarity
es 14; Conserv
                                                                                                                            Sequence 14 AA;
                                                                                                                                                                                                                                                                                                        WO200169261-A2
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                            15-FEB-2002
                                                                                                                                                                                                                                                                                                                     20-SEP-2001
                                                                                                                                                                                                                               ABB55905;
                                                                                                                                                                                                                                                                       Vascular
                                                                                                                                          Query Match
                                                                                                                                                Best Loca
Matches
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(first entry)

Conservative

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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of catters containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of carborophinal fluid (CSF) from the subject one of 223 VD-associated cattering in a sample of creening, diagnosis or prognosis of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABBS5801-ABBS6295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or the effect of therapy administered to a subject at risk of VD. For monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vascular Dementia, VD; VD-associated protein isoform; VPI; screening;
                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular dementia-associated protein isoform (VPI) 110.
                                                                                                                                                                                                                                                                         2.0%; Score 14; DB 4; Ler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; prognosis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB55910 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2000; 2000GB-0006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GSÍQVDGEELVSGR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             619 GSIQVDGBELVSGR
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                                                                                                                                                                                                                                                               Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                         The invention relates to screening, diagnosis or prognosis of Vascular bementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56255) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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100.0%; Pred. No. 6.5e-06;
ative 0; Mismatches 0; Indels
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Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine; immunogenic.

Propionibacterium acnes.

WO2003033515-A1.

Propionibacterium acnes immunogenic polypeptide #30408.

20-OCT-2003 (first entry)

ABM65732;

ABM65732 standard, protein; 159 AA.

RESULT 10 ABM65732

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Gaps

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1 YQLGSGEAR

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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or identifying the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular Dementia, VD; VD-associated protein isoform; VPI; screening; diagnosis; prognosis; gene therapy.
                                                 Query Match 1.4%; Score 10; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 0.041; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Vascular dementia-associated protein isoform (VPI) 109
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1.3%; Score 9; DB 4
Best Local Similarity 100.0%; Pred. No. 0.5
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                      ABB55909 standard; peptide; 15 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 32; 151pp; English.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2001; 2001WO-GB001106.
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                                                                                                                               662 FSSGITGCVK 671
                                                                                                                                                                    1 FSSGITGCVK 10
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                Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                           ABB55909;
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The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

conciding a Propionibacterium acnes protein. The invention also relates to encoding a propionibacterium acnes protein. The invention also relates to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a comprision invention, additionally encompasses expression vectors and host cells comprising a cinvention of the invention, and the invention and isolated T cell population comprising T cells prepared via this method; an isolated T cell population comprising P. acnes polypeptides, polymetric exting a national composition (comprising P. acnes polypeptides, polymetric extension and relative that express the polypeptide, antibodies, fusion proteins, T cell populations, or continuent and method for inhibiting the development of P. acnes in a configuration of action of parient; and method for inhibiting the development of P. acnes in a parient; and method for inhibiting the development of P. acnes in a parient; and method for inhibiting the development of P. acnes in a proteins, T cell populations or antigen-presenting cells that express the composition or antigen-presenting cells that express the polyment of P. acnes in a protein. The polymucleotides an immune response specific for a P. acnes or primers for nucleic acid hybridisation. The vaccine composition is useful for the expression of an immune acid composition is useful for diagnosing a diagnostic assay. The present composition to contain an immuned a page of thought to contain an immuned a contain an immuned a contain an immuned a contain an immuned a contain an immuned a contain an immuned a contain and present of thought to contain an immuned a page in the profession which expenses the polyment of the polyment of the protein in the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the polyment of the pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carter
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Benson DR,
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ic format directly from V
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100.0%; Pred. No. 5.4
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   claim 7; SEQ ID NO 30408; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                             15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2002; 2002WO-US032727
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Best Local Similarity
Matches 9; Conserv
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0; Indels DB 4; Length 15;

587 YOLGSGEAR 595

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548 VRISTASGL 556

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                 Befort K, Costigan M;
                                                                                     Rat Protein CAA40667, SEQ ID NO 9657.
                                        ADE63713 standard; protein; 2531 AA
                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                            14-AUG-2002; 2002WO-US025765.
                                                                      (first entry)
                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
31 VRTSTASGL 39
                                                                                                                                                                                                                                                                 WPI; 2003-268312/26.
                                                                                                                                                                                                                                                 Woolf C, D'urso D,
                                                                                                                             Rattus norvegicus.
                                                                                                                                                                                                                                                                        GENBANK; CAA40667
                                                                                                                                           WO2003016475-A2.
                                                                       29-JAN-2004
                                                                                                                                                           27-FEB-2003
                                                       ADE63713;
                                 ADE63713
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the mucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence witch is differentially regulated in an animal subjected to pain and a chat is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a nagent the expression of a polymucleotide sequence which is differentially subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the sequence for identifying a compound that regulates the activity of one or more of the specification, a method for identifying a compound useful in treating continual a pharmaceutical composition composition composition composition or more polypeptides or their antibodies. The polypeptides given in the sequence presented is a rat protein (end or more of the sequence presented is a rat protein (end or more of the sequence data for identifying a medicament for treating pain, which is patent did not form part of the printed or the sequence data for this patent did not form part of the printed or the sequence data for the specification) but was obtained in electronic form directly from WIPO at the part of the protein contact of the printed or the sequence as a bott of the secuence of the specification of the sequence of the secuence of ftp.wipo.int/pub/published\_pct\_sequences

Sequence 2531 AA;

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence of the polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence that is differentially regulated in a animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence which is differentially expressed in neutronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for pain, a method for identifying a compound or small molecule that regulates the extity in an animal of one or more of the cettod for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the pain and a pharmacentrial commonsiation commonsiance or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or more or mor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Length 2531;
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  DB 7;
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  1.3%; Score 9; DB 7
100.0%; Pred. No. 74;
iive 0; Mismatches
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
        Query Match 1.34
Best Local Similarity 100.0
Matches 9; Conservative
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                                                                                                            466 PCLHGGTCQ 474
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injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

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Gaps

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1.3%; Score 9; DB 7; Length 2531; 100.0%; Pred. No. 74; tive 0; Mismatches 0; Indels

Best Local Similarity 100.0 Matches 9; Conservative

Query Match

Sequence 2531 AA;

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                                                                                                                                                                                                                                             Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                       Gaps
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                                                h 1.3%; Score 9; DB 7; Length 2531; Similarity 100.0%; Pred. No. 74; 9; Conservative 0; Mismatches 0; Indels
                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Befort K, Costigan M;
                                                                                                                                                                                                                          Rat Protein CAA40667, SEQ ID NO 9653.
                                                                                                                                                             ADE63709 standard; protein; 2531 AA.
                                                                                                                                                                                                                                                                                                                                                         14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                       14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                            1029 PCLHGGTCQ 1037
                                                                                         466 PCLHGGTCQ 474
                                                                                                                                                                                                                                                                                                                                                                                                                               Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-268312/26.
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENBANK; CAA40667
                             Sequence 2531 AA;
                                                                                                                                                                                                                                                                                               WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                   27-FEB-2003.
                                                                   Matches
                                                                                                                                           RESULT 13
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a fit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the activity in an animal of one or more of the cativity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in the activity in the polypeptides given in the activity in an animal or one or more of the activity in an animal of one or more of the activity in an animal of one or more of the activity in an animal or or more of the activity in an animal or one or more of the activity in an animal or one or more of the activity in an animal or identifying a compound useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costigan M;
                                                                                                                                                                                                                                                                                                                                                                    Rat Protein CAA40667, SEQ ID NO 9645.
                                                                                                                                                                                              ADE63701 standard; protein; 2531 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                             29-JAN-2004 (first entry)
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                                 1029 PCLHGGTCQ 1037
466 PCLHGGTCQ 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003.
                                                                                                                                                                                                                                                     ADE63701;
                                                                                                                                       RESULT 14
ADE63701
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The invention discloses a composition comprising two or more isolated rate or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of pain animal of one identifying a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

Claim 1; Page; 1017pp; English.

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pain and a pharmaceutical composition comprising the one or more poin and a pharmaceutical composition the polygoticatides or their antibodies. The polygoticatide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction thipty (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 37920.
                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 9; DB 7;
100.0%; Pred, No. 74;
ative 0; Mismatches
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Best Local Similarity 100...
Best Local Similarity 100...
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N-PSDB; ABL14479.
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 2531 AA;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insectiolates, therapeutical and pharmaceutical faruge. The invention discloses genomic DNA sequences (ABLi16.176-ABL30511), expressed DNA sequences (ABL16.176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 37920; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                        Li PWD, Myers EW;
23-MAR-2001; 2001WO-US009231.
                                                                                               23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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1.3%; Score 9; DB 4; Length 3319;

Sequence 3319 AA;

Query Match

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            Gaps
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             0; Indels
 100.0%; Pred. No. 96; ative 0; Mismatches
             9; Conservative
                                                      3033 NDGEWHRVT 3041
                                 603 NDGEWHRVT 611
Best Local Similarity
Matches 9; Conserv
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Search completed: March 9, 2004, 17:27:53 Job time : 88.8465 secs

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Gabs

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0; Indels

Length 2531;

20, Appl 28116, A

16, Appl 18465, A 1, Appli

4170, Ap 7317, Ap 5488, Ap 27759, A 23483, A 21008, A 6672, Ap 28786, A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-644-271-30

Sequence 30, Application US/08644271

Sequence 30, Application US/08644271

Patent No. 1814478

GENERAL INFORMATION:

APPLICANT: Valenzuela, et al.

APPLICANT: Valenzuela, et al.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS

TITLE OF INVENTION: AND LIGANDS

NUMBER OF SEQUENCES: 32

CORRESPENDENCE ADDRESS:

ADDRESSE: APPLICANT Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road

CITY: Tarrytown
US-09-363-316B-3
US-09-621-976-4170
US-09-543-681A-7317
US-09-107-522A-5488
US-09-252-991A-27759
US-09-252-991A-27759
US-09-252-991A-27759
US-09-252-991A-27769
US-09-107-532A-6672
US-08-252-991A-28786
US-08-315-695-20
US-08-315-695-20
US-09-252-991A-28116
US-09-252-991A-18465
US-08-252-991A-18465
US-08-252-991A-18465
US-08-755-559-1
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US-09-252-991A-28324
US-09-252-991A-27099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDSKette
COMPUTER: IDSKette
COMPUTER: IDSKette
COMPUTER: IDSKette
COMPUTER: IDSKette
COMPUTER: IDSKETE
SOFTWARE: FASTEN: DOS
SOFTWARE: TASTEN DATA:
FILING DATE: 10-MAY-1996
CLASSIFICATION NUMBER: USKN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY FASTEN THORMATION:
NAWE: CODERT, RODERT J
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3%; Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1940 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 914-345-7721
TELEX:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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LOCATION: 1...1940
OTHER INFORMATION:
            USA
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STATE: NY
COUNTRY: U
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            Sequence 1, Appli
Sequence 12, Appli
Sequence 4, Appli
Sequence 10, Appli
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Sequence 18061,
Sequence 18061,
Sequence 18061,
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Sequence 34, Appl
                                                                                                                                                                        March 9, 2004, 17:25:24; Search time 27.0475 Seconds (without alignments) 1345.642 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(19072 6/prodata/2/iaa/5B_COMB.pep:*
(20072 6/prodata/2/iaa/6A_COMB.pep:*
(20072 6/prodata/2/iaa/6B_COMB.pep:*
(20072 6/prodata/2/iaa/PcTUS_COMB.pep:*
(20072 6/prodata/2/iaa/PcTUS_COMB.pep:*
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(20072 6/prodata/2/iaa/PcTUS_COMB.pep:*
(20072 6/prodata/2/iaa/PcTUS_COMB.pep:*
(20072 6/prodata/2/iaa/PacKfIlesI.pep:*
                                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-562-702A-6
US-09-562-702B-7
US-08-460-309-4
US-09-125-077-4
US-09-252-917A-18061
US-09-249-697A-3
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US-09-252-991A-19300
US-09-540-236-2071
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US-08-699-232-1

US-09-562-702A-8

US-09-562-702A-8
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US-08-340-428B-49
US-09-230-652-2
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US-09-077-955-34
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US-08-460-309-2
US-08-125-077-2
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Match Length
                                                                 Copyright
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Maximum DB seq
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Perfect score:
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No.
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                 0; Gaps
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                 0; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: PC
OCMPUTER: PC
OPERATING SYSTEM: «UNKNOWM>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 701Y 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 5434, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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COUNTRY: USA
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                                                                     1228 PCLHGGTCQ 1236
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US-09-107-532A-5434
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US-09-077-955-34
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Sequence 2071, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2071
LENGTH: 579
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GENERAL INFORMATION:
Patent No. 6551795

GENERAL INFORMATION:
Patent No. 6551795

GENERAL INFORMATION:
Patent No. 6551795

GENERAL INFORMATION:
PAPPLICANT:
PAPPLICANT:
PATILE OF INVENTION:
PAPPLICANT:
PAPPLICANT:
PAPPLICANT:
PAPPLICANT:
PAPPLICANT:
PAPPLICANT:
PAPPLICANT:
PRIOR FILING DATE:
1999-02-18
PRIOR FILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-07-27

NUMBER OF SEQ ID NOS:
33142
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                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...241
SEQUENCE DESCRIPTION: SEQ ID NO: 5434:
                TELECOMMUNICATION INFORMATION:
TELEPANE: (781)893-807
TELERAX: (781)893-807
TELERAX: (781)893-827
INFORMATION FOR SEQ ID NO: 5434:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOUNCE:
ORGANISM: Enterococcus faecium
REFERENCE/DOCKET NUMBER: GTC-012
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US-09-252-991A-19300
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US-09-540-236-2071
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Sequence 1, Application US/09113825
Patent No. 6149902
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                                                                                                                                             Gaps
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APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Fortini, Mark
APPLICANT: Fortini, Mark
APPLICANT: Mateuro, Kanji
TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH FATHWAY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                               Length 579
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OTHER INFORMATION: Highly conserved ankyrin repeat
CTHER INFORMATION: region of No. 5780300ch
US-08-537-2104.
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Fast SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,210A
FILING DATE: 29-SEP-1995
CLASSIFICATION NUMBER: 18,372
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCKET NUMBER: 7326-027
REFERENCE/DOCKET NUMBER: 7326-027
TELECOMMUTICATION INFORMATION:
TELEFONE: 212-790-9090
TELEFAX: 212-790-9090
TELEFAX: 6644 PENNIE
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 1015 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREN: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08537210A Patent No. 5780300
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TYPE: amino acid
STRANDEDNESS:
                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: protein
                                 ; ORGANISM: M.catarrhalis
US-09-540-236-2071
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Best Local Similarity
Matches 8; Conserva
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10036/2711
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RESULT 7 US-09-113-825-1

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TATES OF INVESTIGNATION AND ADDRESS. Spyridon
APPLICANT MATURAL TRANSHORM SMITH AND APPLICANT FORTILL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL MATURAL
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543 TIELEVRT 550
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Sequence 2, Application US/08125077

Patent No. 5872231 5840863

GENERAL INFORMATION:

APPLICANT: Engvall, Eva

APPLICANT: Lavo, Ilmo

ITILE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

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TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

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TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Encoding Merosin

TITLE OF INVENTION: Nucleic Acids Enc
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1.1%; Score 8; DB 2; Length 1130;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMFUTER: IEM PC compatible
COMFUTER: IEM PC compatible
COMFUTER: IEM PC compatible
COMFUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIPFCATION: 435
PRICK APPLICATION NUMBER: US 08/125,077
FILING DATE: 2-28P-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-3N-1990
PRICK APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 12--UL-1992
APPLICATION NUMBER: US 07/919,951
FILING DATE: 12--UL-1992
APPLICATION NUMBER: US 07/919,951
FILING DATE: (619) 335-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9049
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPRICATION acids
TWDE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 921.2
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . TYPE: amino acid
; TOPOLOGY: linear
; WOLECTLE TYPE: protein
US-08-460-309-2
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California
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2471 amino acids
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Best Local Similarity 100.0
Matches 8; Conservative
                                               Query Match
Best Local Similarity 100.(
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-16
                                                                                                                                                                                  1237 GPSGPRCQ 1244
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                                                                                                                                       483 GFSGPRCQ 490
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US-08-185-432-16
     US-09-230-652-2
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APPLICANT: Tournier-Lasserve, Elisabeth
APPLICANT: Tournier-Lasserve, Elisabeth
APPLICANT: Douted. Anne
APPLICANT: Douted. Anne
APPLICANT: Bach, Jean-Francois
TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
TITLE OF INVENTION: THERAPEUTICATION
FILE REFERENCE: 03715.0048-0000
CURRENT FILING DATE: 1999-05-17
EARLIER APPLICATION NUMBER: W8/09/233
EARLIER APPLICATION NUMBER: R9 6 09733
EARLIER APPLICATION NUMBER: R9 7 04680
EARLIER FILING DATE: 1997-04-16
EARLIER FILING DATE: 1997-04-16
EARLIER FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 163
SOUTHARE: Patentin Ver. 2.1
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1.1%; Score 8; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        COMPUTER: FLOPEN disk
COMPUTER: FLOPEN disk
COMPUTER: FLOPEN disk
COMPUTER: FLOPEN disk
COMPUTER: FLOPEN FC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
FILING DATE: 03 August 1992
FILING DATE: 04 August 1992
FILING DATE: 05 AUGUST 1892
FILING DATE: 05 AUGUST 1892
FILING DATE: 06 AUGUST 1892
FILING DATE: 07 AUGUST 1892
FILING DATE: 08 AUGUST 1892
FILING DATE: 08 AUGUST 1893
FILING DATE: 08 COCKET NUMBER: DATA
FELECOMMUNICATION INPORMATION:
TELEPHONE: 202-737-35-28
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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FEATURE:
OTHER INFORMATION: human ADNc No. 6537775ch 3
                    ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09230652A; Patent No. 6537775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1257 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-340-428B-49
                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 PCLHGGTC 473
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U.S.A.
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LENGTH: 2321
TYPE: PRT
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COUNTRY:
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Sequence 19, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08185432
Patent No. 575052
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buseau, Isabelle
APPLICANT: Buseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Matsumo, Kenji
ITILE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
ITILE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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1.1%; Score 8; DB 4; Length 2321;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZUDING VOIR
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION NUMBER: TS-ESIGN
MAME: MISTOCK, S. Lesie
REGISTRATION NUMBER: T326-006
TELERDANION: 120-9090
TELERAK: (212) 790-9090
TELERAK: (212) 790-9090
TELERAK: (212) 780-8090
TELERAK: 66141 PENNIE:
SEQUENCE CHARACTERISTICS:
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Parent No. 6083904

GENERAL INFORMATION:
APPLICANT: Actavanis-Teakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: Muchelc Acids
NUMBER OF ENQUENCES: 21
CONDESSEDS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
STATE: New York
STATE: New York
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1.1%; Score 8; DB 1; Length 2471;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
REPREMENCE, S. Leslie
REGISTRATION NUMBER: 1326-015
REPREMENCE/DOCKET NUMBER: 7326-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERA: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
TELEX: SEQUENCE CHRACTERISTICS:
CENGTH: 2471 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPACT.

ZUET. 10036
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
TITLE OF INVENTION: Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION WIMBER: 08/083,590
FILING DATE: 25-JUN-1993
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                                                                                                                    CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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US-08-532-384-19
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### ATTORNEY/AGENT INFORMATION:
| NAME: Mistock, S. Lesie
| REGISTRATION NUMBER: 18,872
| REDECOMUNICATION INFORMATION:
| TELECOMUNICATION INFORMATION:
| TELECOMUNICATION INFORMATION:
| TELECOMUNICATION: 12,869864/9741
| TELETRA: 212 869864/9741
| TELETRA: 66141 PENNIE
| INFORMATION FOR SEC IN NO: 19:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 2471 amino acids |
| TOPOLOGY: unknown |
| TOPOLOGY: unknown |
| TOPOLOGY: unknown |
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1228 PCLHGGTCQ 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-190-115-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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                                                                                                                              March 9, 2004, 17:27:59; Search time 51.7431 Seconds (without alignments) 2876.963 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                       1 EIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB_PSP:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_REW_PUB_PSP:*

3: /cgn2_6/ptodata/1/pubpaa/RCT_REW_PUB_PSP:*

4: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.PSP:*

5: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.PSP:*

6: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.PSP:*

7: /cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.PSP:*

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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5 US-10-180-115-29

6 US-09-076-724A-136

US-09-864-761-35784

5 US-10-264-761-35784

5 US-10-264-761-35784

5 US-10-266-829-75

4 US-10-286-829-75

4 US-10-22-706-31

1 US-09-833-245-770

4 US-10-245-107-80

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6 US-10-245-107-80

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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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US-10-238-133-80
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US-10-245-437-80
US-10-245-437-80
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### ALIGNMENTS

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US-10-016-248.34, Application US/10016283

| Sequence 34, Application US/10016283
| Publication No. US20020164702A1
| GENERAL INFORMATION:
| APPLICANT: Valentucia et al., David M.
| TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
| TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
| TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
| FILE REPERENCE: REG155-B-70-103
| FRIOR PRICATION NUMBER: US/09/077,955A
| PRIOR PRILING DATE: 1998-09-10
| PRIOR FILING DATE: 1998-12-13
| NUMBER: OF SEQ ID NOS: 36
| SOFTWARE: PATOR NOS: 36
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APPLICANT: Shimkets, Leil
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Blimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhard
FILE OF INVENTION NUMBER: US/10/369,072
CURRENT APPLICATION NUMBER: 10/174,372
PRIOR APPLICATION NUMBER: 09/989,994
PRIOR PLING DATE: 2000-06-17
PRIOR PPLICAN NUMBER: 60/215,856
PRIOR PPLICANION NUMBER: 60/215,856
PRIOR PPLICANION NUMBER: 60/215,856
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
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PRIOR PLING DATE: 2000-
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US-09-776-724A-136

| US-09-776-724A-136
| Publication No. US20030050455A1
| Publication No. US20030050455A1
| GENERAL INFORMATION:
| TITLE OF INVENTION:
| TITLE REPRENCE: PS.011
| CURRENT APPLICATION NUMBER: US/09/776,724A
| CURRENT PILING DATE: 2001-02-06
| PRIOR APPLICATION NUMBER: 09/69,688
| PRIOR APPLICATION NUMBER: 09/69,688
| PRIOR FILING DATE: 2000-02-08
| PRIOR FILING DATE: 1999-01-14
| PRIOR FILING DATE: 1999-01-14
| PRIOR FILING DATE: 1999-01-14
| PRIOR FILING DATE: 1999-01-14
| PRIOR FILING DATE: 1999-01-14
| PRIOR FILING DATE: 1999-01-14
| PRIOR APPLICATION NUMBER: PCT/US98/14613
| PRIOR APPLICATION NUMBER: PCT/US98/14613
| PRIOR APPLICATION NUMBER: 60/052,661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                    Rastelli, Luca
Grosse, William M
Szerkeres, Edward S
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus norvegicus
US-10-369-072-29
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APPLICANT: Tchernew, Velizar T.
APPLICANT: Tchernew, Velizar T.
APPLICANT: Tchernew, Velizar T.
APPLICANT: Carhusen, Bryan D.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-050 CIP (10) (115)
CURRENT FILING DATE: 2002-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR APPLICATION NUMBER: 60/308,996
PRIOR APPLICATION NUMBER: 60/308,996
PRIOR FILING DATE: 2002-04-01
PRIOR PILING DATE: 2002-06-01
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR PILING DATE: 2000-07-07
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                                                                                                                                                               Lepley, Denise M.
Liu, Xiaohong
Mezick, Amanda J.
Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
Burgess, Catherine E
                                                                                                                                                                                                                                                                                                                                                                                                                     Shenoy, Suresh G.
Shimkets, Richard A.
Spaderna, Steven K.
Spytek, Kimberly, Szekeres, Edward S.,
Taupier, Raymond J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
                                                                Grosse, William M. Susev, Vladimir Y. Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.3
Best Local Similarity 100.
Matches 9; Conservative
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, ORGANISM: Homo sapiens
US-10-190-115-29
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INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8
INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.5
INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.8
INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.8
INFORMATION: EXPRESSED IN BEALN, SIGNAL = 5.8
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.2
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PELING DATE: 2001-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-06-05
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-264-237-2547
; Sequence 2547, Application US/10264237
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-864-761-35784
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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COCATION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LOCATION: (39)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-776-724A-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                             PRIOR APPLICATION UNMER: 60/052,871
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,683
PRIOR FILING DATE: 1997-08-18
                                                                                          ING DATE: 1997-07-16
LICATION NUMBER: 60/052,871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 136
LENGTH: 54
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 VTLLRSLT 81
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Gaps

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RESULT 8
US-10-266-829-75
Sequence 75, Application US/10266829
Publication No. US20030220489Al
GENERAL INFORWATION:
         Best Local Similarity 100.0%;
Matches 8; Conservative 0
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WIHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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LOCATION: (1157)
DIHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE

LOCATION: (127)

COTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

05-10-264-237-2547
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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## Publication No. US2004009491A1
| GENERAL INFORMATION:
| APPLICANT: Birse et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies |
| TITLE OF INVENTION: NUMBER: US/10/264,237 |
| CURRENT APPLICATION NUMBER: US/10/264,237 |
| FRIOR APPLICATION NUMBER: PCT/US01/16450 |
| PRIOR APPLICATION NUMBER: PCT/US01/16450 |
| PRIOR FILING DATE: 2001-05-18 |
| PRIOR FILING DATE: 2000-05-19 |
| PRIOR FILING DATE: 2000-05-19 |
| NUMBER OF SEQ ID NOS: 2876 |
| SOFTWARE: PatentIn Ver: 3.1
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1.1%; Score 8; DB 15; Length 131;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indele
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Publication No. US2004010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFRENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-04-22
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SOUTHARD: PRIOR PREDICATION NUMBER: 60/199, 384
TYPE: PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 2267
SOUTHWARE: PATENTING DATE: 2000-04-25
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SOUTHWARE: PATENTING DATE: 2000-04-25
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SOUTHWARE: PATENTING DATE: 2000-04-25
SOUTHWARE: PATENTING DATE: 2011
SEQ ID NO 2022
LENGTH: 264
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NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
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LENGTH: 131
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Sequence 251, Application US/10219220
| Sequence 251, Application US/10219220
| Publication No. US20030082724A1
| Sequence 251, Application William Sequence 251, Application No. US20030082724A1
| Publican No. US20030082724A1
| APPLICANT: Flinn, Barry
| APPLICANT: Lasham, Annette
| TITLE OF INVENTION: Compositions affecting programmed cell
| TITLE OF INVENTION: Compositions affecting programmed cell
| TITLE OF INVENTION: Compositions affecting programmed cell
| TITLE OF INVENTION: Gaeth and their use in the modification of plant development
| TITLE OF INVENTION: USC 1000-10221
| CURRENT APPLICATION NUMBER: US. No. US20030082724A1 09/325,932
| PRIOR PRILING DATE: 1999-06-04
| NUMBER OF SEQ ID NOS: 290
| SEQ ID NO S: 299
| LENGTH: 299
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1.1%; Score 8; DB 15; Length 264;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: 29 Human secreted proteins
FILE REFERENCE: P2041P1
FILE REFERENCE: P2041P1
FURRENT APPLICATION NUMBER: US/10/266,829
CURRENT FILING DATE: 2002-10-09
FRICR APPLICATION NUMBER: PCT/US00/19735
FRICR APPLICATION NUMBER: PCT/US00/19735
FRICR PILING DATE: 2000-07-20
FRICR APPLICATION NUMBER: 60/145,220
FRICR PILING DATE: 1999-07-23
FRICR FILING DATE: 1999-07-23
SOFTWARE: PATENTIN VET: 2.00
SEQ ID NO 75
LENGTH: 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-829-75
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Gaps ö

0; Indels

Pred. No. 66; 0; Mismatches

278 GVLLFSGG 285

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13 GVLLFSGG 20

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APPLICANT: Scephal, Josen-Fillippe
APPLICANT: Weed, William
APPLICANT: Wood, William
APPLICANT: Pood, William
APPLICANT: Pood, Sherman
APPLICANT: Pood, Sherman
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APPLICANT: Pood, Sherman
APPLICANT: Pood, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMENBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RIC112
CURRENT FILING DATE: 100/197942
PRIOR PRILING DATE: 100/197942
PRIOR PELLING DATE: 1997-00-17
PRIOR PELLING DATE: 1997-10-24
PRIOR PILLING DATE: 1990-00-27
PRIOR PILLING DATE: 1998-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local Similarity 100.0%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches
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; Publication No. US20030068779A1
; GENERAL INFORMATION:
    APPLICANT: Baker, Kevin
    APPLICANT: Baton, Dan
    APPLICANT: Filvaroff, Ellen
    APPLICANT: Goddard, Audrey
    APPLICANT: Gurney, Austin
    APPLICANT: Smith, Victoria
    APPLICANT: Rephan, Jean-Phillippe
    APPLICANT: Rang, Zemin
    APPLICANT: Pong, Sherman
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PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
                                                     tephan, Jean-Phillippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 PCQNGGQC 173
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US-10-245-103-80
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US-10-122-706-31

Sequence 31, Application US/10122706

Publication No. US20030119012A1

GENERAL INFORMATION:

APPLICANT: Stinivaen, Maithreyan

TITLE OF INVENTION: Sulfurylase-Luciferase Fusion Proteins

FILE REFERENCE: 21465-504

CURRENT APPLICATION NUMBER: US/10/122,706

CURRENT FILING DATE: 2002-07-01

PRIOR PRILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 31

LENGTH: 309
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Publication No. US20040010134A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REPREBRICE: PFS.46FCT

CURRENT APPLICATION NUMBER: US/09/833,245

CURRENT FILING DATE: 2000-04-12

PRIOR PAPLICATION NUMBER: 60/250, 358

PRIOR PAPLICATION NUMBER: 60/250, 358

PRIOR PAPLICATION NUMBER: 60/250, 358

PRIOR APPLICATION NUMBER: 60/250, 331

PRIOR APPLICATION NUMBER: 60/250, 384

PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: 60/199, 384

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 2267

SOFTWARE: PALENTIN VEY. 2.1

SEQ ID NO 770

LENGTH: 383
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1.1%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches
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100.0%; Pred. No. 76;
tive 0; Mismatches
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Thermomonospora fusca
US-10-122-706-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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US-09-833-245-770
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### APPLICANT: FORG. SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3630R.LC98

CURRENT PILING DATE: 2002-09-16

PRIOR PILING DATE: 1097-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR FILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-05-22

PRIOR PILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

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PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 80
; SEQ ID NO 80
; LENGTH: 383
; TYPE: PRT
; ORCANISM: Homo Sapien
US-10-245-143-80
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SEQ ID NO 80
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100.0%; Pred. No. 92;
.ive 0; Mismatches 0; Indels
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Pred. No. 92;
Mismatches 0
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean Phillippe
Watambe, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 80, Application US/10245771
Publication No. US20030068781A1
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Best Local Similarity 100.0%;
Matches 8; Conservative 0
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INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
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APPLICANT: Zhang,Zemin
APPLICANT: Eng,Sherman
APPLICANT: Fong,Sherman
APPLICANT: Fong,Sherman
APPLICANT: Fong,Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C90
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 0/063046
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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SEQ ID NO 80
LENGTH: 383
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                                                             PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 66/065027
PRIOR APPLICATION NUMBER: 66/065027
PRIOR FILING DATE: 1999-11-10
PRIOR PELING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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Grimandi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.1%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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US-10-245-107-80
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166 PCQNGGQC 173 ||||||| 100 PCQNGGQC 107

Search completed: March 9, 2004, 17:34:05 Job time: 52.7431 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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9, 2004, 17:23:39; Search time 24.1076 Seconds (without alignments) 2813.016 Million cell updates/sec March Run on:

US-10-006-011A-3
705
1 EIKITFRPDSADGWLLYNGQ......QPLDLQHRAQAGANTRPCPS 705 Title: Perfect score:

Sequence:

Scoring table:

283366 seqs, 96191526 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

Word size :

0

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

virC-region hypoth gene 22 protein - hypothetical prote	さしました	tenebrosin C - sea chemotaxis protein probable transcrip hypothetical prote hypothetical prote equinatoxin II pre	╙╏
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## ALIGNMENTS

	RESULT
_	A38096
_	perlecan precursor - human
	N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate protec
	C; Species: Homo sapiens (man)
_	C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 05-Nov-1999
	C; Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
	R; Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
	J. Biol. Chem. 267, 8544-8557, 1992
	A, Title: Primary structure of the human heparan sulfate proteoglycan from basement membra
	tor, laminin, neural cell adhesion molecules, and epidermal growth factor.
	A;Reference number: A38096; MUID:92235084; PMID:1569102
	A; Accession: A38096
	A;Molecule type: mRNA
	A;Residues: 1-4391 <mur></mur>
	A; Cross-references: GB: M85289; NID: q184426; PIDN: AAA52700.1; PID: q184427
	R; Kallunki, P.; Tryqqyason, K.
	J. Cell Biol. 116, 559-571, 1992
	A; Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD prot
	ell adhesion molecules, and epidermal growth factor.
	A; Reference number: A41736; MUID:92112994; PMID:1730768

A;Accession: S19256
A;Molecule type: mRNA
A;Residues: 1-57, 10', 59-434', A', 436,'FL', 438-449,'Q', 451-502,'A', 503-792,'K', 794-908,'R',
71-2979,'H', 2981-2994,'G', 2996-3167,'T', 3169-3240,'R', 3242-3426,'R', 3428-3631,'Q', 3633-35
A;Cross-references: EMBL:X62815
R;Tryggvason, K.
Submitted to the EMBL Data Library, October 1991
A;Reference number: S77946
A;Accession: S77946

A; Molecule type: mRNA A; Residues: 1.57, 10, 59-434, A, 436, FL', 438-449, Q', 451-502, A', 503-792, K', 794-908, R', 71-2089, H', 2981-2994, G', 2996-3167, T', 3169-3240, R', 3242-3426, K', 3428-3631, Q', 3633-46 A; Cross-references: EMBL: X62515; NID: 929469; PIDN: CAA44373.1; PID: 929470 R; Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K. A; Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the ge A; Reference number: A41059; MUID: 92120660; PMID: 1685141

A; Accession: A41059

A; Molecule type: mRNA
A; Residues: 'RT', 892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 < KA2>
A; Residues: 'RT', 892-908,'R',910-1101,'L',1103-1132,'L',1134-1221,'L',1223-1397 < KA2>
A; Cross-references: GB:S76436; NID:g243370; PIDN:AB21121.1; PID:g243371
B; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, F Genomics 10, 673-680, 1991
A; Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellular A; Reference number: A40306; MUID:91365376; PMID:1679749

A;Molecule type: mRNA A;Residues: 1018-1405,'G',1407-1409,'G',1411-1465 <DOD> A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425 A;Cross-references: A; van der Schueren, B; De Cock, B; Paulsson, M; Cassiman, J.J.; van den J. Cell Biol. 109, 3199-3211, 1989

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Accession: S66460
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                        A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3927 VITPSLSGAGSYLALPALTNIHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVG 3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3807 IPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3987 GHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGL
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 4391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                      A; Reference number: A33625; MUID: 90078352; PMID: 2687294
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 705; DE 100.0%; Pred. No. 0; rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 705; Conservative
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A; Molecule type: mRNA
A; Residues: 940-1601 <NO2>
A; Residues: 940-1601 <NO2>
A; Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A; Accession: B31917
A; Molecule type: mRNA
A; Molecule: 1870-2600 <NO3>
A; Residues: 1870-2600 <NO3>
A; Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
A; Schulze: B:, Mann, K:; Battistutta, R:; Wiedemann, H:; Timpl, R:
Eur. J Biochem 231, 555-556; 1995
A; Title: Structural properties of recombinant domain III-3 of perlecan containing a globn
A; Reference number: 566460; MUID:95377282; PMID:7649154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
S;Species: Mus muscallus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Hau A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogl: adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 < kNO>
A;Residues: 1-3707 < kNO>
A;Cross-references: EmBL: M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
B;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass: A;Itle: Identification of cDNA clones encoding different domains of the basement membran A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
A. Residues: 1272-1274, X', 1276, X', 1278-1279 < SCH>
B. SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB-1284, SUB
                   4166
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                                                                                                                                                                                                                                                                                                                                                                                          600
4107 PCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLC
                                                                                                                                                                                                                       4167 LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV
                                                                                                                                                                                                                                                                                                                                                                                    PETIBLEVRISIASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                           4227 PETIELEVRISTASGLILMWGGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSED
                                                                                                                                         LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4347 RFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 4391
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Best Local Similarity
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F;1807-1959/Domain: laminin G repeat homology <LG3>
$97-116,105-137,171-191,180-212,244-263,252-284,316-335,324-356,389-408,397-429,454-473,
-1476,1483-1494,1488-1504,1506-1515/Digulfide bonds: #status predicted
F;145,672,827,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S18188
R;Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during mammalian development.
A;Reference number: S18188; MUID:92111383; PMID:1764995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    notch protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A; Residues: 1-2511 < WEL:
A; Cross-refreences: EMBL: X57405; NID:g57634; PID:g57635
A; Cross-refreences: EMBL: X57405; NID:g57634; PID:g57635
C; Superfamily: notch protein; ankyrin repeat homology; EGF homology
F; 987-1018/Domain: EGF homology < EGF>
F; 1025-1056/Domain: EGF homology < EGF>
F; 1233-1264/Domain: EGF homology < EGF>
F; 1917-1949/Domain: ankyrin repeat homology < AN1>
F; 1984-2016/Domain: ankyrin repeat homology < AN2>
F; 1984-2016/Domain: ankyrin repeat homology < AN4>
F; 2017-2049/Domain: ankyrin repeat homology < AN4>
F; 2017-2049/Domain: ankyrin repeat homology < AN4>
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                                                                 F;163-212/Domain: Kazal proteinase inhibitor homology «KPI2>
F;236-284/Domain: Kazal proteinase inhibitor homology «KPI3>
F;330-356/Domain: Kazal proteinase inhibitor homology «KPI3>
F;331-429/Domain: Kazal proteinase inhibitor homology «KPI5>
F;346-494/Domain: Kazal proteinase inhibitor homology «KPI5>
F;546-542/Rogion: Kazal proteinase inhibitor homology «KPI6>
F;511-559/Domain: Kazal proteinase inhibitor homology «KPI6>
F;540-542/Rogion: Moror neuron attachment (L-R-B) motif
F;566-645/Domain: Laminin-type EGF-like homology «KPI8>
F;742-786/Domain: laminin-type EGF-like homology «KPI9>
F;842-86/Domain: Razal proteinase inhibitor homology «KPI9>
F;849-992/Region: serine/threonine-rich
F;1147-115/Region: motor neuron attachment (L-R-B) motif
F;1147-115/Region: serine/threonine-rich
F;1147-115/Region: serine/threonine-rich
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1.3%; Score 9; DB 1; Length 1959;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.8
:ive 0; Mismatches
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F;1224-1257/Domain: EGF homology <EG1>
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Best Local Similarity 100.
Matches 9; Conservative
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.; Konstances: 1780-1798 eRUZ>
.; Cross-references: GB:544194
.; Comment: This protein mediates the motor neuron-induced aggregation of acetylcholine rations. This protein mediates the motor constraint labeled below as form 3. Comment: 90% of rat embryonic transcripts encode the variant labeled below as form 3. Superfamily: aggrin, EGF homology; Kazal proteinase inhibitor homology; laminin G repeative splicing; duplication; glycoprocein; neuromuscular junction 7:1-1592. Product: agrin, form 1 #status predicted <AG4>
7:1-1792. Product: agrin, form 3 #status predicted <AG3>
7:1-1779. Product: agrin, form 3 #status predicted <AG3>
7:1-1779. Product: agrin, form 2 #status predicted <AG5>
7:1-1779. Product: agrin, form 2 #status predicted <AG5>
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7:1-1143. Product: agrin, form 2 #status predicted <AG5>
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7:1-1143. Product: agrin, form 2 #status predicted <AG5>
7:1-1143. Product: agrin, form 2 #status predicted <AG5>
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7:1-1143. Product: agrin, form 2 #status predicted <AG5>
7:1-1143. Product: agrin, form 2 #status predict
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NROlecule type: mRNA

NROSacidues: 1-1779,1799-1959 «RUP>

NROSacreferences: GB:M64780; NID:9202798; PIDN:AAA40703.1; PID:9202800

NROSacreferences: GB:M64780; NID:92102798; PIDN:AAA40703.1; PID:9202800

NROSACRET IS uncertain whether Met-1, Met-18, or Met-24 is the initiator

NRUPP, F: Cozcelik, T:: Linial, M.; Peterson, K.; Francke, U.; Scheller, R.

Neurosci. 12, 3535-3544, 1992

NRIPLE: Structure and chromosomal localization of the mammalian agrin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Notch homolog Motch protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 17-Nov-2000
                 Gaps
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R; Reaume, A.G.; Conlon, R.A.; Zirngibl, R.; Yamaguchi, T.P.; Rossant, J. Dev. Biol. 154, 377-387, 1992
A; Title: Expression analysis of a Notch homologue in the mouse embryo. A; Reference number: A48825, MUID:93050801; PMID:1426644
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R;Rupp, F.; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
A;Title: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
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A;Nolecule type: mRNA
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A;Gene: NCSP:13E11.370
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C; Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 07-Mar-2003
C; Accession: A46019; S25144; C41175; B46438; A46438; PH1569; S33109
R; del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gridgenomics 15, 259-264, 1993
A; Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of A; Accession: A46019; MUD:93194170; PMID:8449489
                                                                                                                                                                                                                                                                   A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
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A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
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Cell Biol. 121, 631-641, 1993
Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
Reference number: A46438; MUID:93252998; PMID:8486742
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Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054
Experimental source: embryo
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A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: EMBL:211886
A;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Accession: C49175, MUID:93178563; PMID:8440332
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Experimental source: embryo
Note: sequence extracted from NCBI backbone (NCBIP:126159)
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in; ankyrin repeat homology; EGF homology
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Residues: 1161-1547 < LAR>
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F1063-1094/Domain: EGF homology <EGIS>
F1149-1180/Domain: EGF homology <EGI4>
F1149-1218/Domain: EGF homology <EGI4>
F1187-1218/Domain: EGF homology <EGI4>
F1233-1264/Domain: EGF homology <EGI4>
F1352-1383/Domain: EGF homology <EGI4>
F1351-1425/Domain: EGF homology <EGI5>
F1917-1948/Domain: ankyrin repeat homology <ANI>
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NyAlternate names: protein 13811.370

Species: Neurospora crassa

C;Species: Neurospora crassa

C;Accession: T48789

S;Schulter, U.; Ajgn., V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bubmitted to the Protein Sequence Database, April 2000

A;Reference number: Z24541
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Fitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Experimental source: strain H37Rv
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A; Moderne type: DNA
A; Residues: 1-725. SCCD->
A; Cross-references: EMBL: AL353820; GSPDB:GN00112; NCSP:13E11.370
A; Experimental source: cosmid contig 13E11; strain 74
                                                                                                                                                                                                                                                                                                       Length 2531;
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100.0%; Pred. No. 11;
ative 0; Mismatches
F;1949-1981/Domain: ankyrin repeat homology <AN2>F;1983-2015/Domain: ankyrin repeat homology <AN3-F;2016-2048/Domain: ankyrin repeat homology <AN4-F;2049-2081/Domain: ankyrin repeat homology <AN4-F;2049-2081/Domain: ankyrin repeat homology <AN4-F;2049-2081/Domain: ankyrin repeat homology <AN5-F;2049-2081/Domain: ankyrin repeat ho
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100.0%; Pred. No. 7.6
tive 0; Mismatches
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100.0%; Pred. No. 6.6
live 0; Mismatches
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C,Superfamily: nodulation protein nodP
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C;Species: Bacillus subtilis
C;Date: 00-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C;Date: 00-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C;Accession: F70012
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fubret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galler, C.; Ferrari, E.
Koetter, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kutita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Rose, M.; Sadaie, Y.; Saro, T.; Rieger, M.; Ravolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Saro, T.; Saro, T.; Winters, Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Yanama, H.; Danchin, A.; Tosato, V.; Voshida, K.; Altuhors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tate, K.; Yoshida, K.; Altitle: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID:98044033; PMID:9384377
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 04-Mar-2000
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100.0%; Pred. No. 17;
tive 0; Mismatches
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0; Mismatches
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100.0%; Pred. No
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A;Molecule type: DNA
A;Residues: 1-748 <SHI>
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A;Introns: 329/3; 429/3; 460/2
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les 8; Conserv
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Matches 8,
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R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
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A;Note: Nostoc sp. ptc 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AH2015

F;Kaneko, T.; Nakamura v.; Wollk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                        - Sinorhizobium meliloti (sd
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Experimental source: strain 1021, megaplasmid pSymB bSymB GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
B;Galibert, F:; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Dela, D.; Gonin, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: As6639; MUID:21368234; PMID:11474104
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A;Experimental source: strain PCC 7120
C;Genetics: A11678
A;Gene: a111678
                                                                                                                                                                     conserved hypothetical membrane protein SMb21241 [imported] - Sinorhizobium C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 14;
tive 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
As Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 SYLALPAL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 SYLALPAL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid
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1.1%; Score 8; DB 2
100.0%; Pred. No. 39;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957 PCLHGGTC 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Bxperimental source: embryo
A/Note: sequence extracted from NCBI backbone (NCBIP:126158)
C/Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C/Comment: This protein is one of the neurogenic proteins controlling the decision betwee C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
C;Date: 22-Nov-1995 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000
B;Accention: S;Ratch
J; Maurel, U; Karchikeyan, L; Maurel, P; Margolis, R.U.; Margolis, R.K.
J; Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggrega A;Accession: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Motch B protein - mouse (fragment)
NyAlternate names: Notch homolog
C;Species: Mus musculus (howe mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 08-Sep-2002
C;Accession: A49175; PHIS'0; S32113
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                               A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-886 <GEN>
A/Cross-references: EMBL:299532; PIDN:CAB16720.1; GSPDB:GN00066; SPDB:SPAC7D4.03c
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A;Čross-references: EMBL:X68279; NID:9287989; PIDN:CAA48340.1; PID:9287990
                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC7D4.03c
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C, Accession: T39081
R; Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1997
A; Reference number: Z21826
A; Accession: T39081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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ilarity 100.0%; Pred. No. 38;
Conservative 0; Mismatches
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F;674-705/Domain: EGF homology
F;712-743/Domain: EGF homology
F;836-867/Domain: EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828 VSVNGKRL 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 VSVNGKRL 401
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Best Local Similarity
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482-513/Domain: EGF h
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EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650 complement factor H repeat homology; EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (covalent) #status predicted
                                  Cisuperfamily: aggreean; C-type lectin homology; complement factor H repeat hom Cikeyords: chondroitin sulfate proteoglycan; glycoprotein
Fil-22/Domain: aignal sequence #status predicted <816>
Fil-22/Domain: aignal sequence #status predicted <816>
Fil-257/Product: neurocan #status predicted <816>
Fil-257/Product: neurocan #status predicted <817.
Fil-6-253/Domain: link protein repeat homology <LNX1>
Fil-6-255/Domain: link protein repeat homology <LNX2>
Fil-6-256/Domain: call attachment (R-G-D) motif
Fil-25-1149/Domain: complement factor H repeat homology <FHD>
Fil-6-112/Domain: complement factor H repeat homology <FHD>
Fil-6-1139/737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted Fil-2139/Anding site: chondroitin sulfate (Ser) (covalent) #status experimental
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Gaps

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Length 1257; 0; Indels

DB 2;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:21:48; Search time 17.0517 Seconds (without alignments) 2152.832 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-006-011A-3 705 1 EIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

141681 segs, 52070155 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_42:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		P25304 rattus norv			_	_						-	7 homo		Q04721 homo sapien	ratt	-									_		Q9ylu9 actinia equ	Q93109 actinia equ	1349	P26220 streptomyce	1004
QI.	HUMA	AGRI RAT	NTC1 MOUSE	NTC1_RAT	CYSD MYCTU	AMPA BACSU	PGCN_RAT	PGCN_MOUSE	PGCN HUMAN	AGRI_DISOM	AGRI_CHICK	CRB DROME	NTC3 HUMAN	NTC2 MOUSE	NTC2 HUMAN	NTC2 RAT	LMA2 MOUSE	LMA2 HUMAN	YO09_BPL2	YSCB_YEREN	VG22_BPML5	PTGA_BUCAI	SLYD_TREPA	RS7 THEAC	RS7_THEVO	RR4B CYACA	EQT2 ACTEQ	EQT4_ACTEO	EQTS_ACTEQ	MYB1_NEUCR	XYNC STRLI	YRT2_CAEEL
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% uery atch	1001	9 -		1.3	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.0	1.0	٠		•	•	1.0	•	•	1.0	1.0	•	1.0	•
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Result No.	H (	7 ~	4	S	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q8wvn6 homo sapien P20540 vaccinia vi P07612 vaccinia vi P03040 variola vi P05403 alcaligenes 08322 treponema p 007921 bacillus su C53143 rhodobacter P21914 drosophila P43523 thermus the P56949 rhizobium m Q9feg8 oryza sativ
SCTM HUMAN VLO1 VACCY VLO1 VACCY VLO1 VARY TFDC ALCEU TEDC ALCEU CYCG AHOSH BUSB DROME FWT THETH MUCF RHIME NASZ ORYSA
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### ALIGNMENTS

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                                                                                                                                            | cloning, cellular expression, and mapping of the gene (HSPG2) to                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | "Heparan Bullate proteoglycan of numan colon: partial molecular                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            
                                                                                                                                                                                                                                                 | II H.F., IOZZO K.V.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | bodge G.K., Kovalbzky L., Chu M.L., hdbsell<br>Vi 대 다 Tozzo R V .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | MEDITINE SISSOS (0) FULLMENT (9/49)  Dodge G P Kovelerky T Chi M I. Hassell                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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                                                                                                                                                                                                           | "Perlecan, the major proteoglycan of basement membranes,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Hentati F., Fontaine B.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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MEDLINE-20553141; Pubmeda-11101850; MIGOLE S., DEORING C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TORJUNG C.S., TOR | 467-kD protein containing multiple domains reserve density lipoprotein receptor, laminin, neum molecules, and epidermal growth factor."; J. 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Chem. 267:8544-8557(1992).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 467-kD protein containing multiple domains rese<br>low density lipoprotein receptor, laminin, neum<br>molecules, and epidermal growth factor.";<br>J. 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Homo sapiens (Human). Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute-Manmalia; Butheria; Primates; Catarrhini; Hominidae; Hom(NCBI TaxID=9606; MEDLINE-212094; PubMed=1730768; Kallunki P., Tryggvason K.; MEDLINE-212094; PubMed=1730768; Kallunki P., Tryggvason K.; MEDLINE-212094; PubMed=1730768; MEDLINE-212094; PubMed=150102; Manhin, neural cell amolecules and epidermal growth factor."; J. Cell Biol. 116:559-571(1992). 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MEDINE=2012994; Pubmed=1730768; 261000000000000000000000000000000000000                                                                                                                                                                                                                           | P98160; 016287; 02618.0; 02618.0; 016287; 02618.0; 016287; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0; 02618.0 | P9B160; 016287; 0318287; 0318287; 0318287; 0318287; 0318287; 0318287; 0318287; 0318287; 0318287; 0318282003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last annotation update) Basament membrane specific heparan sulfate prot protein precursor (HSPG) (Perlecan) (PLC). HOMO sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebn Mammalia; Eutheria; Primates; Catarrhini; Homin NCH. TaxID=966; [1]  Kallunki P. Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Taxibasemen membrane haparan sulfate for call Biol. 116:559-571(1992).  SEQUENCE FROM N.A. Skin; MEDLINE-92235084; Pubmed-1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Frimary structure of the human heparan sulfate basement membrane (HSPG/Perlecan). 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HOMO sapiens (Human): Eukaryota; Metazoa; Chordata; Craniata; Vertebi Mammalia; Eutheria; Primates; Catarrhini; Homir NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE-92112994; PubMed=1730768; Kallunki P., Tryggvason K.; MEDLINE-92112994; PubMed=1730768; Kallunki P., Tryggvason K.; MEDLINE-92112994; PubMed=1730768; Kallunki P., Tryggvason K.; Mannan basement membrane heparan sulfate protein wolscules, and epidermal growth factor."; J. Cell Biol. 116:559-571(1992).  SEQUENCE FROM N.A. TISSUE-Colon, and Skin; MEDLINE-92235084; PubMed=1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., "Primary structure of the human heparan sulfate basement membrane (HSPG2/perlecan). A chimeric domains homologous to the low density lipoprote neural cell adhesion molecules, and epidermal J. Biol. Chem. 267:8544-8557(1992). | P9B160; 016287, 09B160; 01627-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Bacement membrane specific heparan sulfate prot protein precursor (HSPG) (Perlecan) (PLC). HOMO sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebn Mammalia; Eutheria; Primates; Catarrhini; Homin NCB. TaxID=966; 1015.  [1] WEDLINE=92112994; Pubmed=1730768; Manualia; Pr. Tryggvason K.; Kallunki P.; Tryggvason K.; Kallunki P.; Tryggvason K.; Kallunki P.; Tryggvason K.; Kallunki P.; Tryggvason K.; Call since protein containing multiple domains restlow density lipoprotein receptor, laminin, neumolecules, and epidermal growth factor."; J. Cell Biol. 116:559-571(1992).  ESCUENCE FROM N.A. TISSUE-Colon, and Skin; MEDLINE=92235084; Pubmed=1569102; Murdoch A.D.; Dodge G.R.; Cohen I.; Tuan R.S., Primary structure of the human heparan sulfate basement membrane (HSPGZ/perlecan). A chimeric domains homologous to the low density lipoprote neural call adhesion molecules, and epidermal. | P98160; 016287; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 02618181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181; 026181;
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HOMO sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebn Mammalia; Eutheria; Primates; Catarrhini; HominOCH TaxID=966; [1]  Kallunki P. Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Kallunki Factor."; J. Cell Biol. 116:559-571(1992).  SEQUENCE FROM N.A. Skin; MEDLINE-92235084; Pubmed-1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Primary structure of the human heparan sulfate basement membrane (HSPG/Perlecan). | P98160; 016287, 0916.09; 016287; 0916.09; 016287; 0916.09; 016287; 0916.09; 016287; 0916.09; 016287; 01627.2003 (Rel. 44, Last sequence update) 10-0CT-2003 (Rel. 44, Last sequence update) Saeament membrane specific heperan sulfate protein precursor (HSPG) (Perlecan) (PLC). HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebn Mammalia; Butheria; Primates; Cararrhini; Homin NGH TaxID=9606; 11]—SEQUENCE FROM N.A. MEDLINE=92112994; Pubmed=1730768; Kallunki P., Tryggvason K.; "Human basement membrane heparan sulfate protector, Expropering membrane heparan sulfate protector, and basement membrane heparan sulfate protector, and epidermal growth factor."; 0. Cell Biol. 116:559-571 (1992). SEQUENCE FROM N.A. TISSUE-Colon, and Skin; MEDLINE=22236084; Pubmed=1559102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Mrimary structure of the human heparan sulfate. | P9816.0; 016287; 0914.07; 101-0CT-1996 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Basement membrane-specific heparan sulfate proteoglycaprotein precursor (HSPG) (Perlecan) (PLC). HORD Sapiens (Human). Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; HNCBI TaxID=9606; 101 SEQUENCE FROM N.A. MEDLINE=92112994; PubMed=1730768; Kallunki P., Tryggrason K.; Human basement membrane heparan sulfate proteoglycan 467-kD protein containing multiple domains resembling low density lipoprotein receptor, laminin, neural ceill molecules, and epidermal growth factor."; 12) SEQUENCE FROM N.A. TISSUES-COLOM, and Skin; MEDLINE=9235084; PubMed=1569102; Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R | P98160; 016287; 029140; 029160; 016287; 029160; 016287; 029160; 016287; 029160; 016287; 029160; 029160; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603 | P98160; 016287; 029140; 0216287; 0216287; 0216287; 0216287; 0216287; 0216287; 0216287; 0216287; 0216287; 0216287; 021628203 (Rel. 4), Last sequence update) 10-0CT-2003 (Rel. 4), Last sequence update) 10-0CT-2003 (Rel. 4), Last annocation update) Basement membrane specific heparan sulfate proteoglycaprotein precursor (HSPG) (Perlecan) (PLC). HSPG2. HOMO sapiens (Human). Eukaryota; Mekazoa; Chordata; Craniata; Vertebrata; EuMammalia; Eutheria; Primates; Catarrhini; Hominidae; HNCB1 TaxID=5666; [1] SQUENCE FROM N.A. MEDIINE-2912994; PubMed=1730768; Kallunki P., Tryggvason K.; Raniman basement membrane heparan sulfate proteoglycan 467-KD protein containing multiple domains resembling now density lipoprotein receptor, laminin, neural cell molecules, and epidermal growth factor."; J. Cell Biol. 116:559-571(1992). SEQUENCE FROM N.A. TISSUE-Colon, and Skin; | P98160; 016287; 029140; 029160; 016287; 029160; 016287; 029160; 016287; 029160; 016287; 029160; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 0291603; 029160 | P98160; 016287; 029140; 029180; 016287; 029180; 016287; 029180; 016287; 029180; 016287; 029180; 029180; 0291803; 010-0CT-1999 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last amoration update) Basement membrane specific heparan sulfate proteoglycaprotein precursor (HSPG) (Perlecan) (PLC). Homo sepiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Erom N.A.  MEDLINE=92112994; PubMed=1730768;  Kallunki P., Tryggvason K.;  Kallunki P., Tryggvason K.;  Kallunki P., Tryggvason K.;  MEDLINE=92112994; PubMed=1730768;  Kallunki P., Tryggvason K.;  Medlinki Diporotein receptor, laminin, neural cell molecules, and epidermal growth factor.";  J. Cell Biol. 116:559-571(1992). | P9816.0; 016287, 02914.0; P9816.0; 016287, 02914.0; 28-FEB-2003 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-CCT-2003 (Rel. 42, Last annocation update) Basement membrane specific heparan sulfate proteoglyca protein precursor (HSPG) (Perlecan) (PLC). HSPG2. HORD sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu Mammalia;
Butheria; Primates; Cararrhini; Hominidae; HNCII TaxID=9606; [1] SQUENCE FROM N.A. MEDLINE-9112994; PubMed=1730768; Kallunki P., Tryggvason K.; "Human basement membrane heparan sulfate proteoglycan 467-KD protein containing multiple domains resembling low density lipoprotein receptor, laminin, neural cell molecules, and epidermal growth factor."; J. Cell Biol. 116:559-571 (1992). | P98160; 016287, 029140; 101-0CT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last sanotation update) Basement membrane-specific heparan sulfate proteoglyca protein precursor (HSPG) (Perlecan) (PLC). HORD: protein Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; HOSI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=92112994; PubMed=1730768; Kallunki P., Tryggrason K.; "Human basement membrane heparan sulfate proteoglycan 467-Kb protein containing multiple domains resembling low density lipoprotein receptor, laminin, neural celling molecules; and epidermal growth factor."; | P9816.0; 016287, 0916.09.  10-0CT-1996 (Rel. 41, Last sequence update)  28-FEB-2003 (Rel. 42, Last sequence update)  10-0CT-2003 (Rel. 42, Last sequence update)  10-0CT-2003 (Rel. 42, Last senocation update)  Basement membrane specific heparan sulfate proteoglyca protein precursor (HSPG) (Perlecan) (PLC).  HSPGD:  HSPGD:  HOME Sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; EuMammalia; Eutheria; Primates; Catarrhini; Hominidae; HNCEI TAXID=9606;  [1]  SEQUENCE FROM N.A.  MEDLINE-2012994; PubMed=1730768;  Kallunki P., Tryggvason K.;  Human basement membrane heparan sulfate proteoglycan 467-KD protein containing multiple domains resembling alow density lipoprotein receptor, laminin, neural celland and contains and celland and celland. | P98160; 016287; 0916387; 0916387; 016287; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 026387; 0263 | P98160; 016287; 0914087; 0916087; 016287; 0264087; 016087; 0267-1996 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last sequence update) Basement membrane specific heparam sulfate proteoglycaprotein precursor (HSPG) (Perlecan) (PLC). Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Bulheria; Primates; Catarrhini; Hominidae; [1] SEQUENCE FROM N.A. MEDLINE-92112994; PubMed=1730768; Kallunki P., Tryggvason K.; Kallunki P., Tryggvason K.; Arakh ryote proteoglycan Afarkh ryote in containing mulfiple domains resembling |                                                       | P98160, Q16287, Q9813V5; 01-OCT-1996 (Rel. 34, Created) 28-PEB-2003 (Rel. 41, Last seq 10-OCT-2003 (Rel. 42, Last ann Basement membrane-specific hep protein precursor (HSPG) (Perl-HSPG). HOMO sapiens (Humn). Eukaryotea, Metazoa; Chordata; Mammalia; Eutheria; Primates; (I) SEQUENCE FROM N.A. | P98160, 016287, C9813V5; 01-0CT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last seq 10-0CT-2003 (Rel. 42, Last ann Basement membrane-specific heg protein precursor (HSPG) (Perl HSPG) HSPG HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Butheria; Primates; I] | P98160, Q16287, Q9813V5; 01-OCT-1996 (Rel. 34, Created) 28-PEB-2003 (Rel. 41, Last seq 10-OCT-2003 (Rel. 42, Last ann Basement membrane-specific her protein precursor (HSPG) (Perl HSPG2. HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606; | P98160, 016287, 0913405; 01-0CT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last seq 10-0CT-2003 (Rel. 42, Last ann Basement membrane-specific hep proctein precursor (HSPG) (Perl HSPG). HOMO sapiens (Human). Eukaryota, Metazoa; Chordata; Mammalia; Eutheria; Primates; | P98160, Q16287, Q9813V5;<br>01-OCT-1996 (Rel. 34, Created)<br>28-FEB-2003 (Rel. 41, Last sec<br>10-OCT-2003 (Rel. 42, Last ann<br>Basement membrane-specific hep<br>protein precursor (HSPG) (Perl<br>HSPG2.<br>Home sapiens (Human).<br>Bukaryota, Metazoa; Chordata;<br>Mammalia: Buthbria: Primates; | P98160, Q16287, Q9813V5, O1-OCT-1996 (Rel. 34, Created) 28-PEB-2003 (Rel. 41, Last seq 10-OCT-2003 (Rel. 42, Last ann Basement membrane-specific her protein precursor (HSPG) (Perl HSPG2. Home specific seq Human). | P98160, 016287, (291345, 01-0CT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last seq 10-0CT-2003 (Rel. 42, Last am Basement membrane-specific heg protein precursor (HSPG) (Perl HSPG: Homo sapiens (Human).    |                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    
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O16287;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 11111111111                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TANDARD; 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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   Its promoter."

Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).

Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).

[ABDLINE-22660472; PubMed=12754519; Annay H., Li X.-J., Martin D.B., Aebersold R.; Abbang H., Li X.-J., Martin D.B., Aebersold R.; Andentification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry."; The "Identification and quantification is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.

C. -- SUBONAT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1- SUBCELLULAR LOCATION: Extracellular.
1- TISSUE SPECIFICITY: Found in the basement membranes.
1- TISSUE SPECIFICITY: Found in the basement membranes.
1- PTM: CONTAINS THERE HEPRRAN SULFATE CHAINS AS WELL AS N-LINKED
2- AND O-LINKED OLIGOSACHARIDES.
2- I- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
2- Grandrome (SJG1) [MIM:255800]; a rare autosomal recessive disorder characterized by permanent myotonia (prolonged failure of muscle characterized by permanent myotonia (prolonged failure of muscle relaxation) and skeletal dysplasia, resulting in reduced stature, Kyphoscollosis, bowing of the diaphyses and irregular epiphyses.
2- SIMILARITY: Contains 4 IDA-receptor class A domains.
2- SIMILARITY: Contains 2 laminin EGF-like domains.
2- SIMILARITY: Contains 3 laminin Like C2-type domains.
2- SIMILARITY: Contains 4 EGF-like domains.
2- SIMILARITY: Contains 1 SEA domain.
                                                                                                                                                                                     [6]
SEQUENCE OF 1-21 FROM N.A.
MEDLINE=94052171; PubMed=8224307;
Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
"Structural characterization of the complete human perlecan gene and
MEDLINE=92120660; PubMed=1685141;
Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
Tryggvason K.;
"Cloning of human heparan sulfate protecylycan core protein,
assignment of the gene (HSPG2) to 1p36.1-->p35 and identification of
a BamHI restriction fragment length polymorphism.";
Genomics 11:389-396(1991).
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InterPro; IPR00742; EGF 2.
InterPro; IPR006209; EGF 7:
InterPro; IPR006210; IEGF.
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EMBL; M85289; AAA52700.1; -.
EMBL; AA448795; CAC18534.1; -.
EMBL; M44283; AAA52699.1; -.
EMBL; S76436; AA82121.2; -.
EMBL; 122078; -; NOT_ANNOTATED_CDS, PIR; A38096; A38096.
HSSP; P00740; 1EDM.
Siena-2DPAGE; P98160; -.
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InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig c2.
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R PROSITE; PS00125; EGF 1; 9.
R PROSITE; PS00186; EGF 2; 6.
R PROSITE; PS00186; EGF 2; 6.
R PROSITE; PS50025; IG_IRR; 22.
R PROSITE; PS50025; IG_IRR; 22.
R PROSITE; PS50025; IG_IRR; 21.
R PROSITE; PS5004; IDLRA, 1; 4.
R PROSITE; PS5004; IDLRA, 2; 4.
R PROSITE; PS5004; IDLRA, 2; 4.
R PROSITE; PS5004; SEA; II.
H PROSITE; PS5004; SEA; II.
H PROSITE; PS5004; SEA; II.
H PROSITE; PS5004; SEA; II.
H PROSITE; PS5004; SEA; II.
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H PROSITE; PS5
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 4.
LG-LIKE C2-TYPE 1.
LAMININ BGF-LIKE 1 (N-TERMINAL).
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 5.
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LG-LIKE C2-TYPE 4.
LG-LIKE C2-TYPE 5.
LG-LIKE C2-TYPE 7.
LG-LIKE C2-TYPE 7.
LG-LIKE C2-TYPE 10.
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InterPro; IPR003596; Ig_v.
InterPro; IPR00034; Laminin_B.
InterPro; IPR00034; Laminin_BGF.
InterPro; IPR000131; Laminin_G.
InterPro; IPR000131; Laminin_G.
InterPro; IPR000131; LDL_receptor_A.
Pfam; Pr00008; BGF; 4.
Pfam; Pr000052; Jaminin_B; 3.
Pfam; Pr00052; Jaminin_B; 3.
Pfam; Pr00053; Jaminin_BGF; 7.
Pfam; Pr00053; Jaminin_G; 3.
Pfam; Pr00055; Jaminin_BGF; 7.
Pfam; Pr00055; Jaminin_B; 3.
Pfam; Pr00057; Jaminin_B; 3.
Pfam; Pr00057; Jaminin_B; 3.
Pfam; Pr00059; Jaminin_B; 3.
SWART; SW00181; EGF; 15.
SWART; SW00181; EGF; 15.
SWART; SW00181; EGF; 15.
SWART; SW00181; EGF; 15.
SWART; SW00181; EGF; 21.
SWART; SW00181; EGF; 22.
SWART; SW00181; Lamis; 3.
SWART; SW00182; Lamis; 3.
SWART; SW00192; Lamis; 3.
SWART; SW00192; Lamis; 3.
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                                                     1 BIKITERPDSADGMILYNGOKRVPGSPTNLANROPDFISFGLVGGRPEFRFDAGSGMATI
                                                                               EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
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                                 Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                 .;
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    100.0%; Score 705; DB 1; Length 4391; 100.0%; Pred. No. 0; cive 0; Mismatches 0; Indels 0
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POGNA MOUSE STANDARD; PRT; 3707 AA.
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
BASEMENT membrane-specific heparan sulfate proteoglycan core
protein precursor (HSPG) (Perlecan) (PLC).
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Query Match
Best Local Similarity 100.0
Matches 705; Conservative
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SECUENCE FROM N.A. TISSUE=Melanoma; MEDLINE=92078153; PubMed=1744087; Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M.,

NCBI\_TaxID=10090;

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DESCRIPTION OF SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.

X MEDLINES 89034101, Pubmed=2972708;

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Yamada Y., Hassell J.R.;
"The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Extracellular.
-1- TISSUE SPECIFICITY: Found in the basement membranes.
-1- TISSUE SPECIFICITY: Found in the basement membranes.
-1- FTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
-1- SIMILARITY: Contains 1 laminin EGF-like domains.
-1- SIMILARITY: Contains 3 laminin IV domains.
-1- SIMILARITY: Contains 15 immunoglobulin-like C2-type domains.
-1- SIMILARITY: Contains 1 Baminin G-like domains.
-1- SIMILARITY: Contains 1 SGF-like domains.
-1- SIMILARITY: Contains 1 SGF-like domain.
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EMBL, J04054; AAA39911.1; ---
EMBL, J04055; AAA39911.1; ---
PIR; 518252; 618252.

PIR; 518252; 618252.

PDB; 1GL4; 28-NOV-01.

MGD; MGI : 96257; HSPG2.

GO; GO:0005604; C: Dasement membrane; IDA.

GO; GO:0005604; C: Dasement membrane; IDA.

GO; GO:0005604; C: Dasement membrane; IDA.

GO; GO:0005604; C: Dasement membrane; IDA.

GO; GO:0005604; C: Dasement membrane; IDA.

GO; GO:0005604; C: Dasement membrane; IDA.

InterPro; IPR000742; EGF 2.

InterPro; IPR000742; EGF 2.

InterPro; IPR000110; IQ-11ke.

InterPro; IPR000103; Laminin, B.

InterPro; IPR0001791; Laminin, GF.

InterPro; IPR0001791; Laminin, GF.

InterPro; IPR0001791; Laminin, GF.

InterPro; IPR0001791; Laminin, Gf. 3.

Pfam; PP00054; Iaminin, Gf. 3.

Pfam; PP00055; Iaminin, Gf. 3.

Pfam; PP00057; Idl recept a; 4.

PFam; PP00057; Idl recept a; 4.

PFam; PP00057; Idl recept a; 4.

PFam; PP00057; Idl recept a; 4.

PFam; PP00057; Idl recept a; 4.

PFAM; PR00051; Laminin, B; 3.

SMART; SM00180; EGF Lam; 7.

SMART; SM00181; Lamin 3.

SMART; SM00281; Lamis; 3.
                                                                                                                             molecule.";
J. Biol. Chem. 266:22939-22947(1991)
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SEQUENCE OF 1777-1801 FROM N.A.
MEDLINE=92407628; PubMed=1326608;
Rupp F., Oezcelik T., Lintal M., Peterson K., Francke U., Scheller R.;
"Structure and chromosomal localization of the mammalian agrin gene.";
J. Neurosci. 12:3538-3544(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryonic spinal cord;
MEDLINE=91222870; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
"Structure and expression of a rat agrin.";
Neuron 6:811-823(1991).
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Pred. No. 4.6e-35;
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AGRI RAT,
          DL-RECEPTOR CLASS A 1.

DL-RECEPTOR CLASS A 2.

DL-RECEPTOR CLASS A 3.

DL-RECEPTOR CLASS A 4.

IG-LIKE C2-TYPE 1.

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 1 (N-TERMINAL).

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 2.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 4 (INCOMPLETE).

LAMININ EGF-LIKE 5 (N-TERMINAL).

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 6.

LAMININ EGF-LIKE 9.

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LAMININ EGF-LIKE 11.

G-LIKE C2-TYPE 6.

IG-LIKE C2-TYPE 9.

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IG-LIKE C2-
                                                                                                                                                                                                                                                                  Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein; Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain; Ecktracellular matrix; EGF-like domain; 3D-structure.

SIGNAL

22 3707 BASEMENT MEMBRANE-SPECIFIC HEPARAN
                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULFATE PROTEOGLYCAN CORE PROTEIN.
SMART; SM00192; LDLa; 4.
SMART; SM00200; SEA; 1.
PROSITE; PS00122; EGF_1; 8.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS50026; EGF_3; 4.
PROSITE; PS50025; EGF_3; 4.
PROSITE; PS50025; LAM G DOMAIN; 3.
PROSITE; PS01204; LAMININ TYPE EGF; 11.
PROSITE; PS50024; LDLRA 1; 4.
PROSITE; PS50024; SEA; 1.
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Frid=VSP 001367.
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Frid=VSP 001368.
V -> VTCD (IN A VARIANT).
NW; 7FEFDFDAFF89CC31 CRC64;
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Missing (In isoform 3).
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KAZAL-LIKE 6.
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KAZAL-LIKE 8.
LAMININ BGF-LIKE 1.
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EGF-LIKE 4.
LAMININ G-LIKE 3.
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                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
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BR EMEL; M64780; AAA40703.1; -

BR EMEL; M64780; AAA40703.1; -

BR EMEL; M64780; AAA40702.1; ALT_INIT.

BR PRE, J10399; AGRT.

BREEPC; IPRO06299; EGF Jike.

BR INCEPPC; IPRO06299; EGF Jike.

BR INCEPPC; IPRO06299; EGF Jike.

BR INCEPPC; IPRO01291; Laminin_G.

BR INCEPPC; IPRO01291; Laminin_G.

BR INCEPPC; IPRO0029; Laminin_G.

BR INCEPPC; IPRO0081; EGF, AGRAIN.

BRAM; PRO0081; EGF, A.

BRAM; SMO2044; Laminin_G; 3.

BRAKT; SMO0204; Laminin_G; 3.

BRAKT; SMO0204; Laminin_G; 3.

BRAKT; SMO0204; Laminin_G; 3.

BRAKT; SMO0201; EGF_AMIN.

BRAKT; SMO0202; EGF_2; 1.

BRAKT; SMO0202; EGF_2; 1.

BRAKT; SMO0202; EGF_2; 1.

BRAKT; SMO0202; EGF_2; 1.

BRAKT; SMO0202; EGF_2; 1.

BRAKT; SMO0202; EGF_2; 1.

BROSITE; PS00225; LAMG DOWAIN; 3.

BROSITE; PS00224; EBA; 1.

BROSITE; PS0024; EBA; 1.

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BROSIT
FUNCTION: Component of the basal lamina that causes the aggregation of acetylcholine receptors and acetylcholine-esterase on the surface of muscle fibers of the neuromuscular junction. SUBUNIT: Binds to laminin. Subscribular LOCATION: Synaptic basal lamina at the neuromuscular
                                                                                                                                                                                                                                                                                                                                                                                           ISOIG=P25304-5; Sequence=VSP_001368;

-1 TISSID SPECIFICITY: Embryonic nervous system and muscle.
-1 DEVELOPMENTAL STAGE: More abundant early in development.
-1 PTM: Contains Heparan sulfate chains as well as N-linked and O-linked oligosaccharidas (By similarity).
-1 SIMILARITY: Contains 9 Kazal-like domains.
-1 SIMILARITY: Contains 1 Saminin SGF-like domains.
-1 SIMILARITY: Contains 1 SEA domains.
-1 SIMILARITY: Contains 1 SEA domain.
-1 SIMILARITY: Contains 3 laminin G-like domains.
-1 SIMILARITY: Contains 3 laminin G-like domains.
-1 CAUTION: It is uncertain whether Met-1, Met-18 or Met-24 is the initiator.
                                                                                                                                                 Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist. Isoforms differ
their acetylcholine receptor clustering activity;
                                                                                                                                                                                                                                                          Name=2;
IsoId=P25304-2; Sequence=VSP_001365;
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ALTERNATIVE PRODUCTS:
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Exp. Cell Res. 204:364-372(1993).

SEQUENCE OF 1659-1673 FROM N.A.

MEDLINE-99364499; PubMed=10437788;

Lee J.S., Ishimoto A., Yanagawa S.I.;

Murine leukemaia provirus-mediated activation of the Notchl gene leads to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";

FEBS Lett. 455:276-280(1999).
                                                                                                                               NTCI_MOUSE STANDARD;
PRT; 2531 AA.
Q01705; Q06007; Q61905; Q9902; Q9QW58; Q9R0X7;
Q01-NOV-1995 (Rel. 32, Created)
O1-NEB-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
(MT14) (p300).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Messerle M., Follo M., Nehls M., Eggert H., Boehm T.;
"Dynamic changes in gene expression during in vitro differentiation of mouse embryonic stem cells.";
[Cytokines Cell. Mol. Ther. 1:139-143(1995).
                                 Gaps
                                                                                                                                                                                                                                                                                                                  Franco del Amo F., Gendron Maguire M., Swiatek P.J., Jenkins N.A., Copeland N.G., Gridley T.; "Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of Drosophila Notch.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
STRAIN=CD-1; TISSUE=Embryo;
MEDLINE=93050801; PubMed=1426644;
                                                                                                                                                                                                                                                                                                                                                                                                                      Reaume A.G., Conlon R.A., Zirngibl R., Yamaguchi T.P., Rossant J., "Expression analysis of a Notch homologue in the mouse embryo."; Dev. Biol. 154:377-387(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 93048835, PubMed=1425352,
Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
Greenspan R.J., McMahon A.P., Gridley T.,
"Expression pattern of Motch, a mouse homolog of Drosophila Notch,
suggests an important role in early postimplantation mouse
                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1161-1547 FROM N.A.
STRAIN=CS7BL/6 X CBA; TISSUB=Embryo;
MEDLINE=93179563; PubMed=8440332;
Lardelli M., Lendahl U.;
"Motch A and Motch B-two mouse Notch homologues coexpressed in a
                               ;
         Length 1959;
                               0; Indels
        DB 1;
      Query Match
1.3%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches
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MEDLINE=93194170; PubMed=8449489;
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Cell Res. 204:364-372(1993).
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                                                    466 PCLHGGTCQ 474
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IsoId=Q01705-2; Sequence=VSP_001402, VSP_001403, VSP_001404;
Note=No experimental confirmation available;
C -1-'TISSUE SPECIFICITY: Highly expressed in the brain, lung and thymus. Expressed at lower levels in the spleen, bone-marrow, spinal cord, evee, mammary gland, liver, intestine, skeletal muscle, kidney and heart.
C -1- DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 dpc By a S.5 dpc highly expressed in presonitic mesoderm at 7.5 dpc By enothelial cells, while much lower levels are seen in the neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in the neuroepithelium, and eveloping whisker follicles.
C -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment NIEO; Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21123790; PubMed=1125752;

A Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S., Akaki N., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S., Okano H., Matsuno K.; Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S., Okano H., Matsuno K.; Hui C.-C., Artavanis-Tsakonas S., Okano H., Matsuno K.; Isakonas M., Matsuno K.; Isakonas M., Matsuno K.; Isakonas M., Matsuno K.; Isakonas M., Matsuno M., Matsuno M., Isakonas M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., Matsuno M., 
                                                                                                                                                                                  Logeat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POST-TRANSLATIONAL PROCESSING.
MEDLINE=21374376; PubMed=11459941;
Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";
Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a
                                                                                                                                                                                                                                                                                              The Notchl receptor is cleaved constitutively by a furin-like
SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND MUTAGENESIS OF 1651-ARG-1654.
MEDLINE-98318619; PubMed-9653148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.; "Murine notch homologs (N1-4) undergo presenilin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
MEDLINE=21523956; PubMed=11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).
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IsoId=Q01705-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH DIX1 AND DIX2
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1029 PCLHGGTCQ 1037

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
ONCH EXTRACELLULAR TRUNCATION.
NOTCH INTRACELLULAR DOMAIN.
EXTRACELLULAR (POTENTIAL).
M GO, GO.0005807; Cintegral to plasma membrane; IC.

RGO, GO.0005815; F.protein binding; IPI.

RGO, GO.0005815; F.protein binding; IPI.

RGO, GO.0005184; P.cell differentiation; IMP.

RGO, GO.0007386; P.cell differentiation; IMP.

RGO, GO.00073819; P.N signaling pathway; IC.

RGO, GO.0007381; P.N signaling pathway; IC.

RGO, GO.0007381; P.N signaling pathway; IC.

RGO, GO.000744; EGF_C.

RICEPPC; IPRO0182; Asx hydroxyl S.

RICEPPC; IPRO0182; Asx hydroxyl S.

RICEPPC; IPRO0183; EGF_II.

RICEPPC; IPRO0183; EGF_II.

RICEPPC; IPRO02049; EGF_II.

RICEPPC; IPRO02049; EGF_II.

REPRC; PRO00023; Ank; 7.

REPRC; PRO0006; EGF_SO.

REPRC; PRO0006; EGF_SO.

REPRC; PRO0101; EGFLOOD.

REPRC; PRO0101; EGFLOOD.

REPRC; PRO0101; EGFLOOD.

REPRC; PRO0104; EGFLOOD.

REPRC; PRO0104; EGFLOOD.

REPRC; PRO0104; EGFLOOD.

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REPRC; PRO0104; EGFLOOD.

REPRC; PRO0104; EGFLOOD.

REPRC; PRO0104; EGFLOOD.

REPRC; ROOTES ROOTES REPRCION; 1.

REPRC; PROSTE; PRO0104; ANK REP REGION; 1.

REPRCSTE; PRO0104; EGF_Z; Z;

REPRCSTE; PRO0104; EGF_Z; Z;

REPRCSTE; PRO0104; EGF_Z; Z;

REPRCSTE; PRO0105; EGF_Z; Z;

REPRCSTE; PRO0105; EGF_Z; Z;

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REPR
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1.3%; Score 9; DB 1; Length 2531;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    EMBL; 211886; CAA77941.1;
EMBL; L02613; AAK14898.1;
EMBL; X68278; CAA48339.1;
EMBL; AJ238029; CA440733.1;
EMBL; X82562; CAA57909.1;
EMBL; X82562; CAA57909.1;
PIR; AG019; A46019
PIR; B49175; B49175.
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative splicing SIGNAL
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TISSUE SPECIFICITY.

WEDLINE=21331789; PubMed=11438922;

REDLINE=21331789; PubMed=11438922;

Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;

"Expression patterns of Notch-DSL signaling system during brain throttonal roles for the Notch-DSL signaling system during brain development.";

"Comp. Neurol. 436:167-181(2001).

"I Comp. Neurol. 436:167-181(2001).

"I FUNCTION: Functions as a receptor for membrane-bound ligands Jagged. Jam Deltal to regulate cell-fate determination. Upon ligand activates and Deltal to regulate cell-fate determination. Upon ligand activates genes of the enhancer of split locus. RPP-Y kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). Acts instructively to control the cell fate determination of CNS multipotent progenitor cells, resulting in astroglial induction and neuron/oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- TISSUE STATE INCITY: Expressed in the brain, kidney and spleen.

Expressed in poetnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. Found in both subventricular and ventricular germinal zones.
-!- DEVELOPMENTAL STAGE: In the embryo, highest levels occur between adupts 12 and 14 and decrease rapidly to much lower levels in the adult.
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honjo T.;
"Notchl and Notch3 instructively restrict bFGF-responsive multipotent neural progenitor cells to an astroglial fate.";
Neuron 29:45-55(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1. SUBDITT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).
-1. SUBCELLUTAR LOCATION: Type I membrane protein. Following protectiveal processing NICD is translocated to the nucleus (By
                                                                            01-NOV-1995 (Rel. 32, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 1 precursor (Notch 1)
NOTCH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21094508; PubMed=11182080;
Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
                                                                                                                                                                                                                                                                                                      TISSUE-Schwann cell;
MEDLINES-2111383; PubMed=1764995;
Weinmaster G., Roberts V.J., Lemke G.;
"A homolog of Drosophila Notch expressed during mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Welnmaster G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93202015; PubMed=1295745;
Walmaster G., Roberts V., Lenke G.;
"Notch2: a second memmalian Notch gene.";
Development 116:931-941(1992)
                                                                                                                                                                                                                                                                                                                                                                                       development.";
Development 113:199-205(1991).
                                           STANDARD;
                                                                                                                                                                                     Rattus norvegicus (Rat).
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RESULT 5
NTC1_RAT
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AC Q07008;
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466 PCLHGGTCQ 474

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Gape

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EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 26, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 28, CALCIUM-BINDING (POTENTIAL).
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EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).
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ANK 2.

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POLY-BLA.

POLY-BRO.

POLY-SER.

CLEAVAGE BY (FURIN-LIKE PROTEASE) (B
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Pred. No. 5;
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LIN/NOTCH 2.
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ilarity 100.0%; Pr
Conservative 0;
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CYSD MYCTU
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which is proceolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EO). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

C-IPM: Phosphorylated (By similarity).

C-IPM: PLASTIY: Contains 3 in/Notch repeats.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL; X55405; CAA40667.1; -.

BR HSP; P00740; 1EDM.

HSP; P00740; 1EDM.

RICEPPO; IRRO00122; Asx hydroxyl_S.

RICEPPO; IRRO00122; Asx hydroxyl_S.

RICEPPO; IRRO00139; EGF_1:

RICEPPO; IRRO00139; EGF_1:

RICEPPO; IRRO00209; BGF_1:

RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RICEPPO; RI
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CALCIUM-BINDING (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 7.
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17474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-M. DOVIS; STRAIN-AF2122/97;
SPECIES-M. DOVIS; STRAIN-AF2122/97;
SPECIES-M. DOVIS; STRAIN-AF2122/97;
GAZDIST T., Elgimeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Aktin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
Proc. Natl. Acad. Sci. U.S.A. 1007/8777-7822(2003).

-I-CATALYIT ACTIVITY: AFF + sulfate = diphosphate + adenylylsulfate.
-I-PATHWAY: First step in the sulfate activation pathway. This
reaction occurs early in the reductive branch of the cysteine
01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) (Sulfate adenylate transferase) (SAT) (ATP-eulfurylase small subunit).
GYSD OR RV1285 OR MTCY373.04 OR MB1316.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                SPECIES=M.tuberculosis; STRAIN=H37Rv; MEDLINE=8925987; PubMed=9634210; Cole S.T., Brosen, P. Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Paskhill J., Garnier T., Churcher C., Harris D., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Barnes E., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kregh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the bloicagy of Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthetic pathway.
-!- SUBUNIT: Heterodimer composed of cysD, the smaller subunit, and cysN (By similarity).
-!- SIMILARITY: Belongs to the PAPS reductase family. CysD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.tuberculosis, STRAIN=CDC 1551 / Oshkosh,
MEDLINE=22206494, PubMed=12218036,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weildman U.A., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00064; -; 1.
InterPro; IPR002500; PAPS reduct.
Pfam; PF01507; PAPS reduct; 1.
Cysteine biosynthesis; Transferase; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE007007; AAK45584.1; -. BX248338; CAD94177.1; ALT INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z73419; CAA97751.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Puberculist; Rv1285; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bourseler L., Brans A., Braum M., Briganell S.C., Eron S.,
RA Codani J.J., Comerton I.F., Coummings N.J., Daniel R.A.,
RA Chois K.M., Codani J.J., Comerton I.F., Cummings N.J., Daniel R.A.,
RA Brian K.D., Errington J., Rabret C., Ferrari E., Foulger D.,
RA Britz C., Fulita M., Fulita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga X., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Kulbert M., Moster P., Coffeau A., Golightly E.J., Lazarevic V.,
RA Kulbert M., Melappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Kumano M.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maule C., Medigue C.,
Redina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Person E., Pujic P., Purnelle B., Rapopott G., Rey M., Reynolds S.,
R Reger M., Ravolde C., Rocha E., Roche B., Rose M., Sadaie Y.,
R Scanlan E., Schleich S., Schroeter R., Scoffone F.,
R Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
R Sekiguchi J., Ramkoshi A., Taraka T., Tarpstra P., Tognoni A.,
R Yoshida K., Yoshikawa H.P., Zumachel E., Yoshikawa H., Danchin A.,
R Yoshida K., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Willer B., Mitters P., Walmacher E., Wangerein E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Zumachen E., Yoshikawa H.P., Subartin B.,
R The Robert E., Wanganchen E., Yoshikawa H.P., Subart S., Kumachen E., Yoshikaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                       16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
PEPA OR BSU32050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
XDb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Arg or Lys, and XDb may be Pro.
-!- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family MI7.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
-I- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                          309 AA; 34888 MW; 75D965D35F1EC284 CRC64;
                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                   500 AA
                                                                                                                        Mismatches
                                                                      Score 8; D
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
                                                                 Query'Match 1.1%; Scc
Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
                                                                                                                                                                     279 VLLFSGGK 286
                                                                                                                                                                                                                  41 VLLFSGGK 48
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Complete proteome SEQUENCE 309 AA
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032106;
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            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                         PIR; F700...

RASP; P0072; 1...

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M17.UPW; -..

RECEP; M18.00813; Peptidase_M17_C.

RECEP; RECOGNIS; Peptidase_M17_N; M1.

RECEP; RECOGNIS; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; RECEP; REC
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J. Cell Biol. 125:659-680(1994).

J. Cell Biol. May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and M-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
115-MR-2004 (Rel. 43, Last annotation update)
Neurocan core protein precursor (Chondrottin sulfate proteoglycan 3)
(245 kDa early postnatal core glycoprotein) [Contains: 150 kDa adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattua.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAINS-SPRGUE-BANALBY, TISSUB-BRAIN;
MEDLINE-92406907; PubMed-1326557,
Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.;
Cloning and primary structure of neurocan, a developmentally
regulated, aggregating chondroitin sulfate proteoglycan of brain.";
J. Biol. Chem. 267:19536-19547(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sed
                                                                                                                                             EMBL; Z99120; CAB15195.1; -. PIR; F70012. F70012. MSSP; P00727; 1LAM. MEROPS; MI7.UPW; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVATLTGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 DVATLTGG 374
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CSPG3 OR NCAN.
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C-TYPE LECTIN.
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS01187; EGF 3; 2.
PROSITE; PS01241; LINK; 2.
Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
EGF-like domain; Calcium; Repeat; DOTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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      InterPro; IPR001012; EGF 2.
InterPro; IPR001081; EGF Ca.
InterPro; IPR001081; EGF Ca.
InterPro; IPR001010; IGT-like.
InterPro; IPR001010; IGT-like.
InterPro; IPR001030; IGT-like.
InterPro; IPR001030; IGT-like.
InterPro; IPR001030; IGT-like.
InterPro; IPR001043; Sushi_SCR_CCP.
Ffam; PF00000; EGF; 2.
Pfam; PF00004; IG; 1.
Pfam; PF00103; IGT-like.
Pfam; PF00103; Xlink; 2.
Pfam; PF00103; Xlink; 2.
PRINTS; PR01265; INTERPEZEII.
PRINTS; PR01265; INTERPEZEII.
PRODM; PF000018; INTERPEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                              MO0445; LINK; 2.
PS00010; ASX HYDROXYL; 1.
PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUSHI
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SMART; SM00034; CLECT; 1.
SMART; SM00179; EGF CA; 1.
SMART; SM04409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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PGCN_HUMAN
ID _PGCN_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 28:405-410 (1995).

-1- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                      (GLCNAC. .) (POTENTIAL).
(XYL. .) (CHONDROTIN SULFATE)
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -: SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-: SIMILARITY: Contains 2 EGF-like domains.
-: SIMILARITY: Contains 2 link domains.
-: SIMILARITY: Contains 1 C-type lectin family domain.
-: SIMILARITY: Contains 1 Sushi (SCR) domain.
-: SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Faessler R., "Structure and chromosomal localization of the mouse neurocan gene.";
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
CSP93 OR NCAN.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 8; DB 1; Length 1257;
100.0%; Pred. No. 27;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=96039250; PubMed=7490074;
Rauch U., Grimpe B., Kulbe G., Arnold-Ammer I., Beier D.,
                                                                                                                                                                                                                                                                        967 967 N-LINKED (GLCNAC, . .) (POTE 1164 1164 N-LINKED (GLCNAC, . .) (POTE 1257 AA; 135544 MW; 992B33DCFA19EEIB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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MGD; MGI:104694; Cspg3.
InterPro; IPR002353; AntifreezeII.
InterPro; IPR00152; Asx_hydroxyl_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Brain.
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Best Local Similarity
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P55066;
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SEQUENCE
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PGCN MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254. Lamerdin J.E., McCready P.M., Skowzonski E., Adamson A.W., Burkhart-Schultz K., Gorden L., Klyle A., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Coeffeld J., Dattix C., Andreise T., Trankhelm M., Amico-Keller G., Coeffeld J., Duarts S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Rogience analysis of an -1 Mb region containing the MEF2B gene in 19912.";
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-1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-1- SIMILARITY: Contains 2 SEP-like domains.
-1- SIMILARITY: Contains 2 link domains.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 C-type lectin family domain.
-1- SIMILARITY: Contains 1 Sushi (SCR) domain.
-1- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
O14594; Q9UPK6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3)
CSPG3 OR NCAN OR NEUR.
                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99013874; PubMed=9795216;
Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G.;
"Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
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SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
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DR SWART; SM00179; EGF_CA; ...

DR SWART; SM00409; IG; 1.

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DR PROSITE; PS00010; ASX HYDROXYL; 1.

DR PROSITE; PS00010; ASX HYDROXYL; 1.

DR PROSITE; PS00022; EGF 1; 3.

DR PROSITE; PS01186; EGF 2; 1.

DR PROSITE; PS01187; EGF 1; 3.

DR PROSITE; PS01187; EGF 2; 1.

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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Basmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
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AC 090404,

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
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R PFEM; PF00008; SEA_GOMAIN.

R PFEM; PF00008; BCF; 1.

R PFEM; PF000053; BAMININ_EGF; 2.

R PFEM; PF000054; BAMININ_EGF; 2.

R PFEM; PF000015; BGP_LAMININ.

R SWART; SW00180; BGP_LAMININ.

R SWART; SW00214; EGF_LAMININ.

R SWART; SW00280; KAZAL; 2.

R SWART; SW00280; EGF_L; 2.

R SWART; SW00280; EGF_L; 2.

R SWART; SW00280; EGF_L; 2.

R PROSITE; PS01086; EGF_L; 5.

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PIR; T43060; T43060.
HSSP; P00740; IEDM.
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1955 AA; 211411 MW; B4DEB27C23422581 CRC64;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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100.0%; Pred. No. 40;
iive 0; Mismatches 0; Indels
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STANDARD; PRT; 2139 AA.

AC P10040;

DT 01-WAR-1989 (Rel. 10, Created)

DT 01-WAR-1991 (Rel. 18, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

CRUMDS protein precursor (95F).

GN CRB.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insection

OC Nooptera; Endopterygota; Diptera; Brachycera; Muc CRB.

ON NCBI_TAXID=7227;

RN SEQUENCE FROM N.A.

RC STRAIN=Oregon-R; TISSUE=Embryo;
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this stitutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SIMILARITY: Contains 3 laminin G-like domains.
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KAZAL-LIKE 6.
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KAZAL-LIKE 7.
KAZAL-LIKE 7.
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LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
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LAMININ G-LIKE 2.
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LAMININ G-LIKE 3.
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EMBL; M97371; AAA48586.1; -.
EMBL; M97372; -; NOT_ANNOTATED_CDS.
PIR; JH0591; AGGCH.
HSSP; P00740; 1EDM.
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InterPro; IPR001991; Laminin G.

R InterPro; IPR001991; Laminin G.

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R FRONTS; PR00010; EGFLADOD.

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MEDLINE=90263104; PubMed=2344615;
Tepass U., Theres C., Knust E.;
"Crumbs encodes an EGF-11ke protein expressed on apical membranes of brosophila epithelial cells and required for organization of cell 61:787-799(1990).
                                                                                                        P SEQUENCE OF 1663-1955 FROM N.A.

C TISSUE=Embryo;

A Wassain H., Campos-Ortega J.A.;

Knust E., Dietrich U., Tepass U., Bremer K.A., Weigel D.,

A Vaesain H., Campos-Ortega J.A.;

EGF homologous sequences encoded in the genome of Drosophila

T melanogascer, and their relation to neurogenic genes.";

EMBO J. 6:761-76(1987).

C PUNCTION: May play a role in the development of epithelia,

Dossibly for the establishment and/or maintenance of cell

C --- FUNCTION: May a ct as a signal.

--- SUBCILULAR LOCATION: Type I membrane protein.

--- SUBCILULAR LOCATION: Type I membrane protein.

--- STMILARITY: Contains 29 EGF-like domains.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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EMBL; X05144; CAA28793.1; --
PIR; A35672; A35672.
PIR; B26637; B26637.
HSSP; P00740; 1EDM.
Flybase; FBgn0000368; crb.
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SEQUENCE FROM N.A.
MEDLINE=97032728; PubMed=8878478;
Joutel A., Corpectot C., Ducros A., Vahedi K., Chabriat H., Mouton P., Joutel A., Corpectot C., Ducros A., Namechal E., Maciazek J., Alamowitch S., Domenga V., Cecillion M., Marechal E., Maciazek J., Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J., Bach J.-F., Bousser M.-G., Tournier-Lasserve E.;
"Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke and dementia.";
Nature 383:707-710(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN STANDARD; PRT; 2321 AA.
MTC3 HUMAN STANDARD; Q9Y6L8;
Q9UM47; Q9UEB3; Q9UPL3; Q9Y6L8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus notch homolog protein 3 precursor (Notch 3).
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-i- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TW) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
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MEDINTB-20264473; PubMeda108003807;
JOUTEAL A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,
Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve E.;
"Splice site mutation causing a seven amino acid Notch3 in-frame deletion in CADASIL.";
Neurology 54:1874-1875(2000).
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DISBASE: Defects in NOTCH3 are associated with cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) [MIM:125310]. CADASIL causes a type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141; ARG-146; CYS-153; CYS-169; CYS-162; ARG-165; SRR-212; GLY-224; TYS-224; CYS-585; CYS-586; CYS-586; CYS-586; CYS-585; CYS-728; CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.

MEDLINE-98049753; PubMed-9388399;
JOURNEL A., CAPACH K., CAPPCHOL C., Troesch A., Chabriat H., Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G., Bach J.-F., Tournier-Lasserve B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in 19p13.1.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                  SEQUENCE FROM N.A.
Lamerdin D.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise
Trankheim M., Amico-Keller G., Coeffield J., Duarte S., Lucas S.,
Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bach J.-F., Tournier-lasserve E.;
'Strong clustering and stereotyped nature of Notch3 mutations in
CADASIL patients.";
Lancet 350:1511-1515(1997).
Gunel M., Artavanis-Tsakonas S.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

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EGF-LIKE 7.

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EGF-LIKE 14.

CALCIUM-BINDING (POTENTIAL).

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MUC2 MOUSE

TTC2 MOUSE

AC 035516; Q06008; Q60941;

AC 035516; Condon (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
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STRAIN=CS7BL/6; TISSUB=Thymus;
Hamada Y., Higuchi M., Tsujimoto Y.;
"Complete amino acid sequence and mutliform transcripts encoded by single copy of mouse Notch2 gene.";
Submitted (UUL-1994) to the EMBL/GenBank/DDBJ databases.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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"Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of tissues.";
Exp. Cell Res. 204:364-372(1993).
[3]
SEQUENCE OF 1765-2153 FROM N.A.
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                                                   NEUROGENIC LOCUS NOTCH HOMOLOG
NOTCH EXTRACELLULAR TRUNCATION
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NOTCH INTRAEBLLULAR DOMAIN (BY
SIMILARITY).
EXTRACELLULAR (POTENTIAL).
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100.0%; Pred. No. 47;
ive 0; Mismatches
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STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
MEDLINE=93178563; PubMed=8440332;
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SIMILARITY: Belongs to the NOTCH family.

SIMILARITY: Contains 31 Early demains.

SIMILARITY: Contains 3 Lin/Notch repeats.

SIMILARITY: Contains 5 ANK repeats.

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InterPro; IPR001110; ANK.

InterPro; IPR001012; Asx hydroxyl_S.

InterPro; IPR001012; Asx hydroxyl_S.

InterPro; IPR001043; EGF_1.

InterPro; IPR001438; EGF_1I.

InterPro; IPR001438; EGF_1I.

InterPro; IPR0012049; Laminin_EGF.

InterPro; IPR0012049; Laminin_EGF.

InterPro; IPR0012049; Notch.

InterPro; IPR0012049; Notch.

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MIM, 125310; -.
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       MEDINE-21374376; PubMed-1145994;

MEDINE-21374376; PubMed-1145994;

MIZUTANI T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;

"Conservation of the biochemical mechanisms of signal transduction
mixed manalian Notch family members.";

"Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members.";

"FUNCTION: Functions as a receptor for membrane-bound ligands
of aggedl, Jaggedl and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with

"RBP-4 kappa and activates genes of the enhancer of split locus.

"RBP-4 kappa and activates genes of the enhancer of split locus.

"RBP-4 kappa and activates genes of the enhancer of split locus.

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"REP-4 kappa and activates genes of the enhancer of split locus.

"REP-4 kappa and activates genes of the enhancer of cell

"SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-

terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                              Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsujimoto Y., "Differential expression of Notchl and Notch2 in developing and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=035516-2; Sequence=VSP 001405;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,
neuroepithelia, somites, optic vesicles and branchial arches, but
                                                                                       MEDINES99386706; PubMed=10393120; Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R., Tsujimoto Y.; Majimoto Y.; Marijani ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality."; Development 126:3415-3424(1999).
              Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                 [6]

MUTAGENESIS OF MET-1699.
MEDLINE=21523956; PubMed=11518718;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Mutine notch homologs (NI-4) undergo presenilin-dependent
                                      "Inhibition of granulocytic differentiation by mNotchl.";
Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
                                                                                                                                                                                     DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
MEDLINE=95333893; PubMed=7609614;
                                                                                                                                                                                                                                        mouse brain.";
Brain Res. Mol. Brain Res. 29:263-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=035516-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                    proteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
 MEDLINE_97075110; PubMed=8917536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the membrane.
PTM: Phosphorylated.
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FT DOWAIN 558 663 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 668 673 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 643 678 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 680 716 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 718 753 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 755 791 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 871 872 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 871 872 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 871 872 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1029 945 EGF-LIKE 24, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1029 1145 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1161 1037 EGF-LIKE 26, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1162 1221 EGF-LIKE 29, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 11223 1260 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1122 1260 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1122 1260 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT DOWAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ENDAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ENDAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ENDAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ENDAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ENDAIN 1165 1221 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT ERPEAT 1181 145 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT REPEAT 1181 145 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL). FT REPEAT 1501 1533 LIN/NOTCH 2. FT REPEAT 1601 1533 LIN/NOTCH 2. FT REPEAT 1601 1533 LIN/NOTCH 2. FT REPEAT 1601 1533 LIN/NOTCH 2. FT REPEAT 1601 1533 LIN/NOTCH 2. FT REPEAT 1601 1533 LIN/NOTCH 2. FT REPEAT 1601 1500 EGF-LIKE 30, Indels 0, Gaps 0, Indels 10, Malaches 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, Indels 10, I
DOMAIN   530   566   EGF-LIKE   14, CALCIUM-BINDING   DOMAIN   568   603   EGF-LIKE   15, CALCIUM-BINDING   DOMAIN   643   678   EGF-LIKE   17, CALCIUM-BINDING   DOMAIN   643   678   EGF-LIKE   17, CALCIUM-BINDING   DOMAIN   755   791   EGF-LIKE   20, CALCIUM-BINDING   EGF-LIKE   20, CALCIUM-BINDING   EGF-LIKE   20, CALCIUM-BINDING   EGF-LIKE   20, CALCIUM-BINDING   EGF-LIKE   21, CALCIUM-BINDING   EGF-LIKE   22, CALCIUM-BINDING   EGF-LIKE   23, CALCIUM-BINDING   EGF-LIKE   23, CALCIUM-BINDING   EGF-LIKE   24, CALCIUM-BINDING   EGF-LIKE   25, CALCIUM-BINDING   EGF-LIKE   25, CALCIUM-BINDING   EGF-LIKE   25, CALCIUM-BINDING   EGF-LIKE   25, CALCIUM-BINDING   EGF-LIKE   25, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BINDING   EGF-LIKE   26, CALCIUM-BI
DOWAIN   530   566   EGF-LIKE   14, CALC
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426 PCQHGATC 433 |||||||||| 1155 PCQHGATC 1162

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Ogicyon rhizobium magmass drosophila Ogfema streptomyce Ognijo homo sapien Og1663 bacillus an Og1663 bacillus an Og1663 bacillus ac O7x2ca geobacillus O74g1 mus musculu O94sx6 homo sapien Og1645 homo sapien Og17c2 arabidopsis O70474 rattus norvalrila musculus o14260 schizosacch Og1666 gallus gall Og166 gallus gall Og166 gallus gall Og166 gallus gall Og166 gallus gall Og166 gallus gall Og160 schizosacch O85jg7 norwalk-lik O89jg10 norwalk-lik O89cgh rattus rubrip
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
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"Proteoglycan expression in the normal rat kidney.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U75305; AAB51124.1;
InterPro; IPR009885; ConA like lec gl.
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1.8%; Score 13; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Perlecan (Fragment).
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TISSUE=Kidney;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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STRAIN=C57BL/6; TISSUE=Brain;

MEDINEE_2538257; PubMed=12477932;

Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A.M., Gibbs R.A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Whiting M.J. Millan M.J. Schalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Mandar A., Schen E.D. Of Eller J.E.,

"Green Eatlon and initial analysis of more than 15,000 full-length human
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             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
01-DRC-2001 (TrEMBLrel. 19, Last annotation update)
03-adenosylmethionine synthase-like protein (Fragment).
Gillichthys mirabilis (Long-jawed mudsucker).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoreleostei;
Goblidae; Gillichthys.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                        MEDINE=21111; PubMed=11172064; Gracey A.Y., Troll J.V., Somero G.N.; Hypoxid-induced gene expression profiling in the euryoxic fish Gillichthys mirabilis."; Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
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01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
5930402A21 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Brain;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
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                                                                                                                                                 NCBI_TaxID=8222;
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SEQUENCE
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Gaps
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STRAIN=C.B-17; TISSUB=Thymus;
Tsuji H., Ishli-obba H., Ukai H., Katsube T., Ogiu T.;
Tsuji H., Ishli-obba H., Ukai H., Katsube T., Ogiu T.;
Tsudiation-induced deletions in the 5' end region of Notchl lead to the formation of truncated proteins and are involved in the development of muse thymic lymphomas.";

Garcinogenesis 24:1-12 (2003).
EMBL, AB100603; BAC77038.1;

Receptor; Transmembrane.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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llarity 100.0%; Fred. No. 20;
Conservative 0; Mismatches 0; Indele
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Submitted (JAN-2003) to the EWBL/GenBank/DDBJ databases EMBL; BCO43114; AAH43114.1; -
GO; GO:0005509; F:ead-clium ion binding; IEA.
GO; GO:0005509; F:eat-clium ion binding; IEA.
InterPro; IPR00152; Asx_hydroxyl_S.
InterPro; IPR001439; EGF_Z.
InterPro; IPR001439; EGF_II.
InterPro; IPR001439; EGF_II.
InterPro; IPR002049; Laminin_GG.
InterPro; IPR001791; Laminin_G.
PERNTS; PR001791; Laminin_G.
PRINTS; PR00119; EGFBLOD.
PRINTS; PR00119; EGFBLOD.
PRINTS; PR00119; EGFBLANINN.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transmembrane receptor Notch1 8
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100.0%; Pred. No. 10;
7ative 0; Mismatches
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SWART; SM00191; EGF CA; 13.
SWART; SM00222; LamG; 3.
PROSITE; PS00010; ASX HYDROXYL; 8.
PROSITE; PS01186; EGF 1; 14.
PROSITE; PS01186; EGF 2; 9.
PROSITE; PS01186; EGF 2; 9.
PROSITE; PS00025; LAM G DOMAIN; 2.
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Q7TQ51;
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PRT; 3367 AA.
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Schellin K.A., Pauley A.M., Nye J.S.;
Schellin K.A., Pauley A.M., Nye J.S.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AF508809; AAM28905.1; --
MGD; MGI:97363; Notchl.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:00073164; P:cell differentiation; IMP.
GO; GO:0007386; P:compartment specification; IMP.
GO; GO:0045944; P:positive regulation of transcription from P. .; IDA.
InterPro; IPR000110; ARK.
InterPro; IPR000121; Ask. hydroxyl_S.
InterPro; IPR000142; EGF_2.
                                                                                                                                                                                                                                                                                                  STRAIN=C.B-17; TISSUE=Thymus;
STRAIN=C.B-17; TISSUE=Thymus;
TBUJi H., Ishli-Obba H., Ukai H., Katsube T., Ogiu T.;
TBUJi H., Ishli-Obba H., Ukai m., Katsube T., Ogiu T.;
TRAdiation-induced deletions in the 5' end region of Notchi lead to the formation of truncated proteins and are involved in the development of mouse thymic lymphomas.";
Garcinogenesis 24:1-12(2003).
EMBL; AB100603; BAC77039.1; -.
Receptor; Transmembrane.
SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;
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STRAIN=BALB/c; ITSSUE=Thywus;

MEDLINE=55044925; PubMed=7956922;

Nye J.S., Kopan R., Axel R.;

Nya J.S., Kopan R., byptresses neurogenesis and myogenesis but not gliogenesis in mammalian cells;

Development 120:2421-2430(1994).
                                                                                                                                                     Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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STRAIN=BALB/c; TISSUE=Thymus;
STRAIN=BALB/c; TISSUE=Thymus;
MEDLINE=22119593; PubMed=12123574;
Foltz D.R., Santiago M.C., Berechid B.E., Nye J.S.;
"Glycogen Synthase Kinase-3beta Modulates Notch Signaling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 11; Length 2526;
Pred. No. 20;
0; Mismatches 0; Indele
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Curr. Biol. 12:1006-1011(2002).
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STRAIN=C.B-17; TISSUE-Thymus;
Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;
Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;
Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;
Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;
Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogiu T.;
Carcinogenesis and selections in the selection of nouse thymic lymphomas.";
Carcinogenesis 24:1-12(2003).
ENBL; AB100603; BAC77040.1; -.
Receptor; Transmembrane.
SEQUENCE 2531 AA; 270832 MW; 97C91F69BABF02BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1,10EL_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00004; NL; 3.

PROSITE; PS5008B; ANK REPEAT; 4.

PROSITE; PS50029; ANK REP REGION; 1.

PROSITE; PS00100; ASX HYDROXYL; 22.

PROSITE; PS00116; EGF 2; 27.

PROSITE; PS01187; EGF 2; 27.

PROSITE; PS01187; EGF CA; 21.

PROSITE; PS01187; EGF CA; 21.

PROSITE; PS01187; EGF CA; 21.

ANK repeat; EGF 11ke domain; Repeat.

SEQUENCE 2531 AA; 270819 MW; 7DB7E0DEF799D999 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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1.3%; Score 9; DB 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches
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100.0%; Pred. No. 20;
tive 0; Mismatches
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; EGF_II.
InterPro; IPR00209; EGF_II.
InterPro; IPR002019; Iaminin_EGF.
InterPro; IPR002019; Iaminin_EGF.
InterPro; IPR000800; Notch.
InterPro; IPR000800; Notch.
Fam; PF00002; EGF; 36.
Fam; PF00002; EGF; 36.
Fam; PF00001; EGF; 36.
FRINTS; PR0010; EGFELOD.
PRINTS; PR01452; NOTCH.
SWART; SW00181; EGF; 37.
SWART; SW00181; EGF 28.
EGF 28.
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Gaps

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Indels

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Pred. No. 26; Mismatches

100.08;

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Conservative
              Best Local Similarity
Matches 9; Conser
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A CELLIKET S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
A Celliker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesdiolka L., Doyle C.M.,
A Farfan D.E., Galle R., George R.A., Herris N.L., Hoskins R.A.,
A Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotann M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
A Nixon K., Pacleb J.M., Park S., Pfedfer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirekas R.R., Wan K.H., Weinburg T., Zhang R.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AR135118; AAA31714.1;
R EMBL, AR203409; AAR44861.1;
R HSSP; P00740; IEDM.
R Flybase; FBgno004002; wb.
                                                                                                                                                                                                                                                                                                                                             Martin D., Zusman S., Li X., Williams E.L., Khare N., DaRocha S., Chiquet-Ehrismann R., Baumgartner S.; "wing blister, a new Drosophila laminin alpha chain required for cell adhesion and migration during embryonic and imaginal development."; J. Cell Biol. 145:191-201(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., Harriss N., Hartzell G., Harvey D., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw R Celniker S., Rubin G.M.,
An exploration of the sequence of a 2.9-Mb region of the genome of Drosphila melanogater: the Adh region.";
                                                                                          Laminin AlPHA1, 2 (SYMBOL-MB).
WB OR WING BLISTER OR CG12SAB.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoprerygota; Diptera; Brachycera; Muscomorpha;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374097 MW; EB125654B1BC1511 CRC64;
                 U.NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Laminin ALPHA1, 2 (SYMBOL=WB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0007267; P:cell-cell signaling; NAS. InterPro; IPR001589; Actbind actnin.
InterPro; IPR001589; Actbind actnin.
InterPro; IPR00209; EGP like.
InterPro; IPR00034; Laminin B.
InterPro; IPR001791; Laminin EGF.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Laminin G.
Pfam; PF00052; laminin B; 2.
Pfam; PF00053; laminin B; 2.
Pfam; PF00054; laminin G; 4.
Pfam; PF00055; laminin G; 4.
Pfam; PF00055; laminin Ntern; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
MEDLINE=99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                   STRAIN=OREGON-R;
MEDLINE=99207061; PubMed=10189378;
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SMART; SM00282; LamG; 5.
SMART; SM00136; LamNT; 1.
PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00122; EGF 1; 14.
PROSITE; PS01186; EGF 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics 153:179-219(1999).
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Length 3367;

DB 5;

Score 9;

1.3%;

Query Match

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RAMILINE-COINGROOF, PubMed=10731132,

RAMILINE-COINGROOF, PubMed=10731132,

RAMILINE-COINGROOF, PubMed=10731132,

RAMILINE-COINGROOF, PubMed=10731132,

RAMILINE-COINGROOF, PubMed=10731132,

RAMILINE-COINGROOF, RAMILIAGES, Abblunner M., Hedderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RAMILIA, Lewis S.E., Richards S.C., Amblunner M., Hedderson S.N.,

RAMILIA, Dovle C., Rayers Y.H., Blazel R.G., Champe M., Pfeitfer B.D.,

RAMILIA, Dovle C., Baxter E.G., Helt G., Nalson C.R., Gabor G.L.

RAMILIA, Beau A., Basendale C., Baytaktaroglu L., Bealsley E.M.,

RAMILIA, Becon K.Y., Benges P.V., Barnan B.P., Bhandari D., Bolshakov S.,

RAMILIA, Bocchan M.R., Bould C., Davenhoot L., Bolshakov S.,

RAMILIA, Cawley S., Dahlke C., Davenhoot L., Dolez S.M.,

RAMILIA, Cawley S., Dahlke C., Davenhoot L., Diez S.M.,

RAMILIA, Cawley S., Dahlke C., Davenhoot L., Diez S.M.,

RAMILIA, Cawley S., Dahlke C., Davenhoot L., Diez S.M.,

RAMILIA, B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RAMILIA, R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RAMILIA, R., Bungellsta C.C., Ferraz C., Ferriaca S., Felsechman W.,

RAMILIA, M., Hauten A.E., Garg N.S., Gelbart W.M., Glasser K.,

RAMILIA, M., Hauten M., Houten M., Moleson D.L.

RAMILIA, M., Malush P., Karaft C., Kravitz S., Kulp D., Lai Z.,

Alali M., Kalush F., Karaft C., Kravitz S., Kulp D., Lai Z.,

Lu X., Mattei B., McInton R.T., Gunzer D., Morrison J.A., Machen D.L.,

RAMILIA, M., Mauphy B., Murphy L., Murzhy D.M., Nelson D.L.

RAMILIA, M., Maynah R., Miron K., Morison M., Stupski M.P., Shen H.,

RAMILE S., Spradding A.C., Stapleton M., Stupski M.P., Shen H.,

RAMILE S., Spradding A.C., Stapleton M., Stupski M.P., Shu E.,

Syleras R., Zaveri J.S., Zhan M., Raling W., Weissenbach J.,

RAMING S., Woodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RAMILIA, RAMING S., Wasarman D.A., Weinston G.C., The Stupski M. S., Zhon M., Raling S., Zhon M., Raling S., Zhon M., Raling S., Zhon M., Raling S., Zhon M., Raling S., Zhon 
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Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Godson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,

Ferriera S., Frise E., Galle R.F., Garg N.S.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TFEMBLrel. 23, Created)
01-MAR-2003 (TFEMBLrel. 23, Last sequence update)
01-MAR-2003 (TFEMBLrel. 23, Last sequence update)
01-OCT-2003 (TFEMBLrel. 25, Last annotation update)
01-OCT-2003 (TFEMBLrel. 25, Last annotation update)
01-OCT-2003 (TFEMBLrel. 25, Last annotation update)
01-OCT-2003 (TFEMBLrel. 25, Last annotation update)
02-OCT-2003 (TFEMBLrel. 25, Last annotation update)
07-OCT-2003 (TFEMBLrel. 25, Last annotation update)
07-OCT-2003 (TFEMBLrel. 23, Last annotation update)
07-OCT-2003 (TFEMBLrel. 23, Last annotation update)
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07-OCT-2003 (TFEMBLrel. 23, Last anno
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603 NDGEWHRVT
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=36329;
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Best Local Similarity 100.0
Matches 8, Conservative
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QBBMIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Photanenavorg S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003643; AAN10875.1; --
EMBL; AE003643; AAN10875.1; --
EMBL; AE003643; AAN10875.1; --
EMBL; AE003643; AAN10875.1; --
ENBL; AE003643; AAN10875.1; --
ENGLOGO OF CONTROL SEPTIMENTY.

INTERPRO; IPRO06219; ACTAININ B.
INTERPRO; IPRO06319; Laminin B.
INTERPRO; IPRO06319; Laminin B.
INTERPRO; IPRO06319; Laminin B.
INTERPRO; IPRO0631; Laminin GGF.

INTERPRO; IPRO0631; Laminin GGF.

R Pfam; PRO0055; laminin GGF, 14.
R Pfam; PRO0055; laminin Nterm; 1.
R Pfam; PRO0055; laminin Nterm; 1.
R SWART; SW0018; EGFLAMININ.
SWART; SW0018; EGFLAMININ.
SWART; SW0028; Lami, 17.
R SWART; SW0028; Lami, 17.
R SWART; SW0028; Lami, 17.
R PROSITE; PS00029; ACTIN 1; 1.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
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R PROSITE; PS00029; LAMIN TYPE EGF; 16.
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R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
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R PROSITE; PS00029; LAMIN TYPE EGF; 16.
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R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PROSITE; PS00029; LAMIN TYPE EGF; 16.
R PANT TYPE EGF; 16.
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R PANT TYPE EGF; 
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1.3*; Score 9; DB 5; Length 3375;
Best Local Similarity 100.0*; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels
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Q81718;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-UDN-2003 (TrEMBLrel. 24, Last annotation update)
tRNA intron endonuclease, putative.
PF14 O514.
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ACTAINS—22225705; PubMed=12368864; ACTAINS—20225705; PubMed=12368864; ACTAINS—20225705; PubMed=12368864; ACTAINS—20225705; PubMed=12368864; ACTAINS—20225705; PubMed=12368864; ACTAINS—20225705; PubMed=12368864; ACTAINS—2025705; PubMed=12368864; ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—2025705; PubMed=10. ACTAINS—20
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Forelimb;

RA The FANTOM Consortium,

RA The FANTOM Consortium,

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Meakly similar to neurogenic locus notch 3 protein (Fragment).
Wha musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Musinae;
MUSE_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score.8; DB 5; Length 97; 100.0%; Pred. No. 12; ative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 8; Conservative
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01-JUN-2003
01-OCT-2003
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Best Local S
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Q842M1
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Q8G4F5
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                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 19718 / IFO 14298;
STRAIN=ATCC 19718 / IFO 14298;
STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemilthoautotroph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773 (2003).
EMBL; BX321859; CAD84767.1;
GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
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Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
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Bukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                         1.1%; Score 8; DB 11; Length 219;
100.0%; Pred. No. 25;
tive 0; Mismatches 0; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Ali353820; CAB88665.2; --
HSSP; P30086; 1BD9.
219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;
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Pfam; PF01161; PBP; 1.
SEQUENCE 244 AA; 26745 MW; EEB0DC9E6245012A CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phosphoadenosine phosphosulfate reductase (EC 2.7.7.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Related to putative lipid binding protein TFS1.
                                                                                                                                                                                                                                                                                                                                                                                                                244 AA
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100.0%; Pred. No. 27;
tive 0; Mismatches
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                    Local Similarity 100.
hes 8; Conservative
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                                                                                                                                                                                     482 PGFSGPRC 489
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SEQUENCE
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                                                         Query Match
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09P6X9
10 09P6X
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GO; GO:0004781; F:sulfate adenylyltransferase (ATP) activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IPR002500; PaPS_reduct. IEA. Fini, PR01507; PAPS_reduct. IEA. Fini, PR01507; PAPS_reduct. IEA. Nucleocidyltransferase; Transferase; Complete proteome. SEQUENCE 302 AA; 34973 MM; 5499EAC71EF9F7DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds in Rhodococcus sp. strain DS7.";
Submitted (FRB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY244763; AA089190.1;
GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
GO; GO:004781; F:sulfate adenylyltransferase (ATP) activity; IEA.
GO; GO:0004781; F:sulfate adenylyltransferase (ATP) activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
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NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodococcus sp. DS7.
Bacteria, Actinobacteridae, Actinomycetales,
Corynebacterinese, Nocardiaceae, Rhodococcus.
NCBI_TaxID=227347;
                                                                                                                                                                                                                                                     DB 16; Length 302;
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Pfam, PR01507; PAPS_reduct.1.
Nucleotidyltransferage, Transferage.
SEQUENCE 308 AA; 35136 MM; AE64C09A9D453F7C CRC64;
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Probable ribokinase.
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STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
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RA Schell M.A., Karmirantzou M., Shel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RT The genome sequence of Biffdobacterium longum reflects its adaptation
RT The genome sequence of Biffdobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RD SMEL, ABC014773; AND5228.1;
RMEL, ABC014773; AND5228.1;
RMEL, ABC014773; AND5228.1;
RMEL, ABC014773; Pribokinase activity; IEA.
DR GO; GO:006014; Pirbokinase activity; IEA.
DR InterPro; IPR002139; Ribokinase.
DR InterPro; IPR002139; Ribokinase.
DR RINTS; PR00294; PfkB; I.
DR PROSITE; PS00583; PFKB KINASES.1; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 320 AA; 33130 MW; 28F44619036EFC6B CRC64;
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SQ SEQUENCE 320 AA; Mismatches 0; Indels 0; Gaps

QV 325 GRWHRVSA 332
DD 249 GRWHRVSA 256
Search completed: March 9, 2004, 17:30:33
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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March 9, 2004, 17:15:33 ; Search time 24.1076 Seconds (without alignments) 2813.016 Million cell updates/sec

US-10-006-011A-3 3825 1 BIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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317	316	314.5	311	311	304	302.5	302.5	299.5	298	296	296	292	291	287.5	284.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1 A38096 portlecan precursor - human NyAlternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate protei C;Species: Homo sapiens (man) C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 05-Nov-1999 C;Date: 07-Apr-1994 #sequence revision 57-Apr-1994 #text change 05-Nov-1999 C;Date: 07-Apr-1994 #sequence revision 67-Apr-1994 #text change 05-Nov-1999 C;Mocession: A38096; S19256; S77946; A41059; A41036; B33525; A33625; A41736	A.Title: Primary Structure of the human heparan sulfate proteoglycan from basement membr. A.Title: Primary structure of the human heparan sulfate proteoglycan from basement membr. tor, laminin, neural cell adhesion molecules, and epidermal growth factor. A.Reference number: A38096, MUID:92235084, PMID:1569102 A.Mocession: A38096 A.Molecule type: MRNA.	A; Residues: 1-4391 <mur> A; Residues: 1-4391 <mur> A; Cross-references: GB: WB5289; NID: g184426; PIDN: AAA52700.1; PID: g184427 R; Kallunki, P.; Trycgrason, K. J. Cell Biol. 116, 559-571, 1992 A; Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro: ell adhesion molecules, and epidermal growth factor. A; Reference number: A41736; WUID: 92112994; PMID: 1730768 A; Accession: S19256.</mur></mur>	A;Rosidues: 1-57 'D', 59-434,'A', 436,'FL',438-449,'Q',451-502,'A',503-792,'K',794-908,'R', 71-2979,'H',2981-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-33-37,'T',2979,'H',2981-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-33-33-37,Tyggvason, K. R;Tyggvason, K. R;Tyggvason, K. R;Meference number: S77946 A;Reference number: S77946 A;Reference number: S77946 A;Reference number: S77946	A;Rolecules: 1-57, 'D', 59-434, 'A', 436, 'FL', 438-449,'Q', 451-502,'A',503-792,'K',794-908,'R', 71-2979,'H', 2981-2994,'G',2996-3167,'T',3169-3240,'R',3242-3426,'R',3428-3631,'Q',3633-4, A,Cross-references: EMBL:X62515; NID:929469; PIDN:CAA44373.1; PID:929470 R;Kallunk', P.; Eddy, R.L.; Byers, M.G.; Restilae, M.; Shows, T.B.; Tryggvason, K. Genomics 11, 389-396, 1991	Aritie: Cloning of human heparan sulfate proteoglycan core protein, assignment of the granterence number: A41059; MUID:92120660; PMID:1685141 A; Accession: A41059 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA	A; Crossreferences: Tx; 7, 272-1339; CrAz.> A; Crossreferences: Tx; 7, 272-1339; CrAz.> A; Crossreferences: GB: 576436; NID: 9243370; PIDN: AAB21121.1; PID: 9243371 B; Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo, I Genomics 10, 673-680, 1931 A; Title: Heparan sulfate protecglycan of human colon: partial molecular cloning, cellula: A; Reference number: A40306; MUID: 91365376; PMID: 1679749 A; Accession: A40306 A; Molecule type: mRNA A; Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 < DOD> A; Residues: GB: A64283; NID: 9184424; PIDN: AAA52699.1; PID: 9184425 B; Heremans, A; van der Schueren, B; De Cock, B; Paulsson, M.; Cassiman, J.J.; van den J. Cell Biol. 109, 3199-3211, 1989

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A; Accession: S18252
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                                            A.Reference number: A33625, MUID:90078352; PMID:2687294
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C.G.Coession: B361-1236-1
C.S.Uperfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G reper S.22-4331/Domain: ainal sequence #status predicted caids
F.22-4331/Domain: along: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: A.M.Coession: B.M.Coession: B.M.Coession: A.M.Coession: B.M.Coession: B.M.Coession: A.M.Coession: B.M.Coession:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F/3886-3880/Domain: EGF homology <EGF1>
F/3888-3921/Domain: EGF homology <EGF>
F/3888-3921/Domain: EGF homology <EGF>
F/3953-4106/Domain: EGF homology <EGF2>
F/417-4175/Domain: EGF homology <EGF2>
F/419-4151/Region: motor neuron attachment (L-R-E) motif
F/419-4151/Region: motor neuron attachment (L-R-E) motif
F/419-4151/Region: motor neuron attachment (L-R-E) motif
F/55,71,76/Bhinding site: heparan sulfate (Ser) (covalent) #status predicted
F/89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (coval
A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclona
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F;1613-1668/Domain: lam.
F;1673-2686/Domain: IV.
F;2007-2034/Domain: tran.
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NiAlternate names: perjectan
Cispecies: Mus musculus (house mouse)
Cjate: 11-Jan-1995 #sequence_train 11-Jan-1995 #text_change 05-Nov-1999
CjAccession: 818252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha A;Title: The Complete sequence of perlecan, a basement membrane heparan sulfate proteogladhesion molecule.
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A; Residues: 1-370; ANO.>

A; Residues: 1-370; ANO.>

A; Cross-references: EMBL: H77174; NID: 9200295; PIDN: AAA38911.1; PID: 9200296

R; Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass

B; Blol. Chem. 263, 16379-16389, 1988

A; Title: Identification of cDNA clones encoding different domains of the basement membra

A; Reference number: A92680; MUID: 89034110; PMID: 2972708
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:3464-3492/Domain: EGF homology <EGF7>
:1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted
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;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin
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1299-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
1285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
1325-359/Domain: LDL receptor ligand-binding repeat homology <LDL2>
1368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
1764-811/Domain: LDL receptor ligand-binding repeat homology <LDL4>
1764-811/Domain: laminin-type EGF-11/ke homology <LDL4>
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Pred. No. 3.9e-209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPGFSGPRCQQGAGYGVVESD#HPEGSGGNDAPGQYGAYFYDNGFLGLPGNSFSRSLPEV 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3544 PETIEFEVRISTADGLLLWQGV-VREASRSKDFISLGLQDGHLVFSYQLGSGEARLVSGD 3602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3603 PINDGEWHRITALREGGRGSIQVDGEDLVTGRSPGPNVAVNTKDIIYIGGAPDVATLTRG 3662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1779;1799-1959 «RUP>
A; Cross-references: GB: M64780; NID: 9202798; PIDN: AAA40703.1; PID: 9202800
A; Cross-references: GB: M64780; NID: 9202798; PIDN: AAA40703.1; PID: 9202800
A; Experimental source: embryonic spinal cord
A; Note: it is uncertain whether Met-1, Met-18, or Met-24 is the initiator.
B; Rupp, F; Oezcellik, T.; Linial, M.; Peterson, K.; Francke, U.; Scheller, R.
A; Title: Structure and chromosomal localization of the mammalian agrin gene.
A; Feference number: A38856; MUID: 92407628; PMID: 1326608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CiSpecies: Rattus norvegicus (Norway rat)
CiDate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 17-Nov-2000
CiDates: 31-Mar-1999, A38856
CiRccession: JH0399, A38856
R;Rupp, F.; Payan, D.G.; Magill-Solc, C.; Cowan, D.M.; Scheller, R.H.
Neuron 6, 811-823, 1991
A;Fitle: Structure and expression of a rat agrin.
A;Reference number: JH0399; MUID:91222570; PMID:1851019
A;Reference number: JH0399
                                                  3185 YICVCPAGFTAAAVNIRKPCTATP-SLWADATCVNRPDGRGYTCRCHLGRSGVRCEEGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3364 NLHTLIYLGGVEPSVQLSPATNMSAHFHGCVGEVSVNGKRLDLTYSFLGSQGVGQCYDSS
                                                                                                     RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA
                                                                                                                                                                         121 IPKAGLSSGFIGCVRELRIQGERIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESSS
                                                                                                                                                                                             3125 IPKAGLSSGFVGCVRELRIQGEEIVFHDVNLTTHGISHCPTCQDRPCQNGGQCQDSESSS
                                                                                                                                                                                                                                              181 YVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYICRCHLGRSGLRCEEGVT
                                                                                                                                                                                                                                                                                                                VTTPSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVG
                                                                                                                                                                                                                                                                                                                                                                                     GHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGL
                                                                                                                                                                                                                                                                                                                                                                                                              GHLEFRYELGSGLAVLRSHEPLALGRWHRVSAERLNYDGSLRVDGGRPVLRSSPGKSOGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSS
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Indels
 40;
Mismatches
33;
Conservative
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A/Cross-references: GB:544194

G/Croment: This protein mediates the motor neuron-induced aggregation of acetylcholine r C/Comment: D0% of rate embryonic transcripts encode the variant labeled below as form 3. Croment: 90% of rate embryonic transcripts encode the variant labeled below as form 3. ylcholine receptor clustering activity.

G/Superfamily: agrin, EGF homology; Kazal proteinase inhibitor homology; laminin G repea C/Keywords: alternative eplicing; duplication; glycoprotein; neuromuscular junction E/F1-1959/Product: agrin, form 3 #status predicted AGG>

E/1-1959/Product: agrin, form 3 #status predicted AGG>

E/1-1779,1789-1959/Product: agrin, form 5 #status predicted AGG>

E/1-1779,1789-1959/Product: agrin, form 5 #status predicted AGG>

E/1-1779,1789-1959/Product: agrin, form 5 #status predicted AGG>

E/1-1779,1789-1959/Product: agrin, form 5 #status predicted AGG>

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E/1-1779,1789-1959/Product: agrin, form 5 #status predicted AGG>

E/1-1779,1789-1959/Product: agrin, fo
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Fil147-1215/Region: motor neuron attachment (L-R-E) motif
Fil147-1215/Region: motor neuron attachment (L-R-E) motif
Fil147-1215/Region: BGF homology <EG2>
Fil144-1416/Domain: BGF homology <EG2>
Fil144-1416/Domain: BGF homology <EG3>
Fil185-1716/Domain: BGF homology <EG4>
Fil181-1747/Domain: BGF homology <EG4>
Fil181-1747/Domain: BGF homology <EG4>
Fil181-1747/Domain: Laminin G repeat homology <EG3>
Fil1807-116,105-137,171-191,180-212,244-263,252-284,316-335,324-356,389-408,397-429,454-473
Fig7-116,105-137,171-191,180-212,244-263,252-284,316-335,324-356,389-408,397-429,454-473
Fil476,1483-1494,1488-1504,1506-1515/Disulfide bonds: #status predicted
Fil476,672,827,957/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Best Local Similarity 31.5%; Pred. No. 4.6e-47;
Matches 241; Conservative 92; Mismatches 278; Indels 154; Gaps
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Best Local Similarity 30.6%
Matches 221; Conservative
          Kazal
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A/Rolecule type: mRNA

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Cippecies: Gallus gallus (chicken)
Cipate: 31-Mar-1993 #sequere revision 31-Mar-1993 #text_change 17-Nov-2000
CiAccession: JHC591, A38857; B38857; I50692
Riffsim, K. W. K.; Ruegg, M.A.; Escher, G.; Kroeger, S.; McMahan, U.J.
Meuron 8, 677-689, 1992
Afrite: cDNA that encodes active agrin.
A;Reference number: JHO591; MUID:92232297; PMID:1314620
                                                 454 CEHEENPCQLREPCLHGGTC---QGT-RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGG
                                                                                                                                                                                                                                                            -- ELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPI
                                                                                                                                                   510 NDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV------PETI------
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1922 AYGTGFVGCLRDVVVGH-----RQLHLLEDAYTKPELRECFT 1958
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                                                                                                  ----LGNPCLNGGSCVPREATYECLCPGGFSGLHCEKGL---
.686 VSLRGHQL-----LTQEHVLRAVDVSPFADHPCTQA-
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Fig. 1917 Domain: Kazal proteinase inhibitor homology kRP16>
Fig. 1918 John Ann. Kazal proteinase inhibitor homology kRP16>
Fig. 1918 John Ann. Kazal proteinase inhibitor homology kRP16>
Fig. 1918 John Ann. Kazal proteinase inhibitor homology kRP18>
Fig. 1918 John Ann. I aminin-type EGF-like homology kRP18>
Fig. 1918 John Ann. I aminin-type EGF-like homology kRP19>
Fig. 1918 John Ann. Kazal proteinase inhibitor homology kRP19>
Fig. 1918 John Serine/threonine-rich
Fig. 1918 John Ann. EGF homology kEG1>
Fig. 1919 John Ann. EGF homology kEG1>
Fig. 1919 John Ann. EGF homology kEG2>
Fig. 1919 John Ann. EGF homology kEG2>
Fig. 1919 John Ann. EGF homology kEG3>
Fig. 1911 John Ann. EGF homology kEG3>
Fig. 1911 John Ann. EGF homology kEG3>
Fig. 1919 John Ann. EGF homology kEG3>
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Fig. 1919 John Ann. EGF homology kEG3>
Fig. 1919 John Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : ||||
1716 HPCTQKPNPCQ-----NGGTCSPRLESYECACQRGFSGAHCEKVIIEKAAGDAEA1AFD 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1770 GRIYMEYHNAVIKSPDA-----LDYPAEPSEKALQS--NHFELSIKTEATQG 1814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       452 DLCEHEENPCQLREPCLHGGTC---QGTRCLCLPGFSGPRCQQ-----GSGHGIA-- 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALRE 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYP-DYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 I--PKAGLSSGFIGCVR------ELRIQGEEIVFHDLNLTAHGISHC--PTCRDRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 KDGSLRVNGGRPVLRSSPGKSQG-----LNLHTLLYLGGVEPSVPLSPATNMSAHFRGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ESDWHLEGSGGNDAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1689 QRISIKGVPL-----LKEQHIRSAVEIST------
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B47648; C47

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-244,'R','KRXH','S1369,'GN',3372-3373,'G',3375,'RLRHRRNAQNGPLSRKTRTTTKLFGSW
A;Cross-references: EMBL:293375; PIDN:CAB07567.1; GSPDB:GN00020; CESP:ZC101.2a
A;Experimental source: clone C38C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-2441, R', KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRNAQNGPLSRKTRTTTKLFGSW
Residues: 1-2441, R', KRKH', 3369, 'GN', 3372-3373, 'G', 3375, 'RLRHRRNAQNGPLSRKTRTTTKLFGSW
Residues: EMBL: 293395, PIDN: CABO7706.1; GSPDB: GN00020; CESP: ZC101.2a
Recession: T27489
Scatus: preliminary; translated from GB/EMBL/DDBJ
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;Molecule type: DNA;
;Residues: 1-1694,"H', 1883-2441,"R',"KRKH',3369,"GN',3372-3373,"G',3375,"RLRHRRRNAQNGPL:
;Cross-references: EMBL:29375; PIDN:CAB07568.1; GSPDB:GN00020; CESP:ZC101.2c
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[Cross-references: EMBL:293395; PIDN:CAB07704.1; GSPDB:GN00020; CESP:ZC101.2b
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
];Rogalski, T.M.; Williams, B.D.; Mullen, G.P.; Moerman, D.G.
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A,Molecule type: DNA
A,Residues: 1-546,'P',548-2198,'D',2290,'NAR',2294,'L',2296,'WHATE',2302-2303,'V',2305,'I
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Cross-references: EMBL:293395; PIDN:CAB07707.1; GSPDB:GN00020; CESP:ZC101.2c
Experimental source: clone ZC101
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A;Cross-references: GB:L13458
A;Accession: B47648
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                                                                                                                                                                                                                                                              hypothețical protein ZC101.2e - Caenorhabditis elegans
C;5pecies: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence revision 15-0ct-1999 #text change 23-Sep-2002
C;Accession: T19821; T19819; T19820; T27490; T27488; T27489; T27487; A47648;
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A;Molecule type: DNA
A;Residues: 1-3375 <WIL>
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Molecule type: DNA
Residues: 1-3375 <W12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                          R;Baynes, C.
submitted to the EMBL Data Library, March 1997
Kefference number: Z19182
A;Accession: T19821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubmitted to the EMBL Data Library, March 1997
1, Reference number: Z20375
1, Accession: T27490
                                                                                                           -- QELQLVEDALNNPTILHCPA 1326
                                              684 PPOPLDLOHRAQAGANTRPCPS
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Accession: T27488
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 17-Nov-2000
C;Accession: T43060
R;Smith, M.A.; Magill-Solc, C.; Rupp, F.; Yao, Y.M.M.; Schilling, J.W.; Snow, P.; McMaha
submitted to the EMBL Data Library, September 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule Lype: mRNA.
*Residues: 1-1328 -SML.
*Residues: 1-1328 -SML.
*Cross-references: EMBL:L01423; NID:g213102; PID:g213103; PIDN:AAA49224.1
*Superfamily: agrin, EGF homology; Kazal proteinase inhibitor homology; laminin G repea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYG-- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 -AIPKAGLSSGFIGCVRELRIQGEEIVFHDIN-----LTAHGISHCPT--CRDRPCONG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         508 GGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEA 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GRSGLRCE-----EGVTVTTPSLSGAGSYLALPAL----TWTHHELRLDVEFKPLAPD 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895 GREGELCERVSEAEQDQGKAFIPEFNGL-SYLEMNGIHTFVSDLLQKLSMEVIFLAKDPN 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 GVILFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 DGSLRVW-----GGRPVLRSSPGKSQGLNLHTLLYLGGVRPSVPLSPATNMSAHFRGCV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 GEVSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 GQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEE 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    722 SKTLIKPGNWHHVVGNRNRRSGMLSVDGEPHLIGESPPGTDGLNLDTDLFLGGTPRDEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 GQCHDSESSSYVCVCPAGFTGSRC--EHSQALHCHPEACGPDATCVNRPDGRGYTCRCHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
17.4%; Score 667; DB 2; Length 1328;
Best Local Similarity 27.0%; Pred. No. 6.2e-35;
Matches 200; Conservative 112; Mismatches 304; Indels 126; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IKITERPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1072 QKLSLK----SIPLLKKENIRNAMEIS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                            - electric ray (Discopyge ommata) (fragment)
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A)Residues: 1-1715 <USH>
A)Residues: 1-1715 <USH>
A)ACTOSS-references: GS:N96376; NID:9205714; PIDN:AAA41707.1; PID:9205716
A;ACTOSS-references: GS:N96376; NID:9205714; PIDN:AAA41707.1; PID:9205716
A;Note: authors translated the codon GAC for residue 1464 as Thr and ACC for residue 146
R;Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Sudhof, T.C.
B;Ushkaryov, Y.A.; Petrenko, A.G.; Geppert, M.; Sudhof, T.C.
A;Description: Neurexins: Synaptic cell surface proteins related to the alpha-lotrotoxin A;Reference number: S27884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the alpha-latrotoxin recep
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A;Molecule type: mRNA
A;Residues: 1-1666, CRK', 1670, PREEKLLPG',1683-1685, GL',1688, LDLA',1694-1695, CCVCRCRA
A;Cross-references: EMBL:M96376; NID:G205714; PIDN:AAA41706.1; PID:g205715
        37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LHCHPEACGPDATC--- 213
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                                                                                                                                   VSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPL
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                                                                                                                                                                                 3293 VDGRSTGILAMLAVDGNIFVGGVPDISKATGGLFSNNFVGCIADVELNGVK-
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11.0%; Score 421; DB 2; Length 1715;
Best Local Similarity 21.6%; Pred. No. 5e-19;
Matches 193; Conservative 114; Mismatches 274; Indels 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurexin II-alpha precursor - rat
Gispeciae: Rattus norvegicus (forway rat)
Gibate: 21-41-1995 #sequence revision 21-Jul-1995 #text_change
Gibate: 21-41-1995 #sequence revision 21-Jul-1995 #text_change
Gibate: 21-31-1992 #sequence revision 21-Jul-1995 #text_change
Rivelharyov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A;Title: Neurexins: synaptic cell surface proteins related to th
A;Reference number: A40228; MUID:92320296; PMID:1621094
A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                           689 DLQHRAQAGANTRPC 703
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A;Residues: 1-546, P',548-1128,1290, DFARNSPS',1299, NSS',1303-1304, R', RHR',1544-1545,
A;Cross-references: GB:L13458.
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : | | :: | :: | 3.833 SDYGSNTKQYTSLSLIANQVV------LTVRRPDKEVQKIRSETLEAGEL-IDVAVR 2883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2884 QAGNALVMIVDGNQVSTIETDTLKRGTEIFIGGLPPGLN-SPDDVVEQSFQGCVXEILIN 2942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMATIRHPTPLALGHFHTVTLLRSLTQGSLIVGDLA------PVNGTSQGKFQGLDLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2665 RPVFIGGRHE-----PTNEANDFRGIISQVVLSGHNVGLGDARIPSSVVKYDACASTNLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGGQCHDSES-SSYVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYICRC
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            <R02>
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13.4%; Score 511; DB 2; Length 3375;
cal Similarity 20.9%; Pred. No. 1.8e-24;
179; Conservative 140; Mismatches 332; Indels 204; Gaps
,'ANIV',2516-2517,'LQQG',2522,'IDG',2526,'S',2528,'SRGFHV',2535,'F'
'Cross-references: GB:L13458
                                                                                                                              sequence not shown
                                                                                                                              acid
                                          A,Cross-references: GB:L13458
A;Accession: C47648
A;Status: preliminary; nucleic
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02 CEDRPOGNGGCHDSESSSYUCYCPAGFTGSRCEHSOALHCHPEACGPDATC-VNRPDGR 220	Cy 673 LVLESARPGAPP 684    :::	Query Match         10.6%; Score 405.5; DB 2; Length 1530;           Best Local Similarity 20.5%; Pred. No. 4.4e-18;         10.6%; Pred. No. 4.4e-18;           Matches 203; Conservative 112; Mismatches 285; Indels 391; Gaps 42;           Qy         2 IKITFRPDSADGMLX-NGQKRVPGSPTMLANRQPDFISFGLVGGRPEFFFDAGSGMATI 60           b         527 ISPDFRTTERNGLILFSHGKPRHQKDAKHPQMIKVDFFALEMLDGHLYLLDMGSGTIK 586           Qy         61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDL-APVNGTSGGKFQGLDLNEELYLG 113           i
Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Color   Colo	RESULT 8 T42218 Nilt-1 protein homolog - rat Nilt-1 protein homolog - rat Nilt-1 protein homolog - rat Nilt-1 protein homolog - rat Nilt-1 protein homolog - rat C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Species: Rattus norvegicus (Norway rat) C;Accession: T42218 R;Näkayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. R;Title: Inductification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: Z14126, MUID:98360089; PMDI:9693030 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1531 <nak> A;Residues: 1-1531 <nak> A;Residues: 1-1531 <nak> A;Residues: 1-1531 <nak> A;Cross-references: ENBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G3449290 A;Experimental source: strain Sprague-Dawley; brain C;Genetics: A;Gene: mEGP4 C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein r</nak></nak></nak></nak>	Matches 173; Conservative 78; Mismatches 245; Indels 245; Gaps 32;  QY 25 GSPTNIANPOPDFISCHUGGR-PERF

:M96374; NID:g205710; PIDN:AAA41704.1; PID:g205711

ָר ני		A;Residue	s: 1~1507 <ush:< th=""></ush:<>
3 (		C, Superfa	mily: neurexin;
ት 8	180PICKORFCQNGQCGDBESSSXYCVCFFGFGSCCE	F;1-30/DC F;31-1507	F;1-30/Domain: signal se F;31-1507/Product: neure
à	196HSQA	F;680-712 F;1087-11	/Domain: EGF hc 19/Domain: EGF
QC	::  755 PVVMHTEAEDVSLRFRSQRAYGILMATTSRDSADTLRLELDAGRVKLTVNLDCIRINCNS 814	Query Match	fatch Los Similarity
ò	208GPDATCVNRPDGRGYTCR	Matches	202; Conserv
qq	:     SKGPETLFAGYNLNDNEWHTVRVVRRGKSLKLTVDDQQAMTGQMAGDHTRLEFHNIETGI 874	ò	2 IKITFRPDSA
ò	226CHL-GRSGLRCEBGVTVTT 243	QQ	504 ISFDFRTTE
qq	875 ITERRYLSSVPSNFIGHLQSLIFNGMAYIDLCKNGDIDYCELNARFGFRNILADPVTFKT 934	ò	61 RHPTPLAL
δ	LIFSGGKSGPVEDFVSLAMVGG	qq	564 KALQ
· 2	935 KSSYVALATL-QAYTSMHLFPQFKTTSLDGLILYNSGDGNDFIVVELVKGYL 985	È	114 GYPDYGAIPI
ò	304 EFRYELGSGLAVLRSAEPLALGRWHRVSAERLINKDGSLRVNGGRPVLRS 352	qq	617 GLPEN
Ωþ	986 HYVFDLGNGANLIKGSSNKPLNDNQWHNVMISRDTSNLHTVKIDIKITTQITAG 1039	Š	160PTCR1
δ	353 SPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGS 410	g	673 SRETAKPCLA
Db	1040ARNLDLKSDLYIGGVAKETYKSLPKLVHAKEGFQGCLASVDLNGRLPDL 1088	Š	196HSQA
ò	411 QGIGQCYDSSPÇERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCFHEENPCQLREPCLHG 470	qq	732 PVVMHTEAE
ДÞ	1089ISDALFCNGQIERGCEGPSTTCQ-EDSCSNQ 1118	È	208GPDATCV
ò	471 GTCQGTRCLC-LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGA 518	đ	792 SKGPETLFA
QQ	1119 GVCLQQWDGISCDCSMTSFSGPLCNDPGTTYIFSKGGGQITYKWPPNDRPSTRA- 1172	λō	226
à	519 YFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLIWQGVEVGEAGQGKDFIS 575	qq	852 ITERRYLSS
đ	1173DRLAIGFSTVQXEAVLVRVDSSSGLGDYLE 1202	ò	244 PSLSGAGSY
ò	576 LGLODGHLVFRYOLGSGEARLVSEDP-INDGEWHRVTALREGRRGSIQVDGEELVS 630	q	912 KSSY
q	1203 LHIHQGKIGVKFNVGTDDIAIBESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPA 1262	ð	304 EFRYELGSG
ò	631 GRSPGPNVAV 650	QΩ	-9
Ор	: : :       : : :	ò	353 SPGKSQGLN
È	651	q	1017ARNLD
Ωp	1323 LYYNGLKVLNMAAENDANIAIVGNVRLVGEVPSSMTTESTATAMQSEMSTSIMETTTTLA 1382	Š	411 QGIGQCYDS
8	675 IHSARPGAPPPOPLDLOHRAQAGANTRPCPS 705	ପୁ	1066ISDA
Ωp	1383 TSTARRGKPPTKEPVSQTTDDILVASAECPS 1413	ò	471 GTCQG
		QQ	1096 GVCLQQWDG
RESULT A40228	10	ò	519 YFHDDGFLA
neurex. C;Speci		셤	1150 DRLAIG
C, Date C, Acces	-1995 #rext	Ğ	576 LGLQDGHLV
R;Ushka Science	.; Suednor, T.C.	q	1180 LHIHQGKIG
A;Title A;Refer	s: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep rence number: A40228; MUID:92320296; PMID:1621094	<b>&amp;</b>	631 GRSPGPNVA
A;Acces A;Statt	A;Accession: A40228 A;Status: preliminary; nucleic acid sequence not shown A;Aciatus: prope: mRNA	d d	1240 GNNDNERLA
STORIES '	unte cypa: munn		

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cadherin-related tumor suppressor precursor - fruit fly (Drosophila melanogaster)
Cispecies: Drosophila melanogaster
Cipate: 30.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
CiAccession: A41087; B41087
Rimahoney, P.A.; Weber, U.; Onofrechuk, P.; Biessmann, H.; Bryant, P.J.; Goodman, C.S.
Airle: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadhe:
Airle: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadhe:
Airle: The fat tumor suppressor gene in Drosophila encodes a novel member of the cadhe:
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                                                                                       A, Residues: 1-1523 <NAK>
A, Residues: 1-1523 <NAK>
A, Cross-references: EMBL:AB011531; NID:93449291; PIDN:BAA32461.1; PID:93449292
C, Genetics: AGGRES
A, Gene: MEGRES
C, Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
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C;Superfanily: cadherin-related tumor suppressor; cadherin repeat homology; EGF
C;Keywords: cadherin-related tumor suppressor; transmembrane protein
C;Keywords: calcium binding; cell adhesion; duplication; transmembrane protein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-447/Product: cadherin-related tumor suppressor #status predicted <MAT>
F;36-458/Domain: cadherin repeat homology <CR1>
F;151-156/Domain: cadherin repeat homology <CR2>
F;21-382/Domain: cadherin repeat homology <CR3>
F;390-494/Domain: cadherin repeat homology <CR3>
F;390-494/Domain: cadherin repeat homology <CR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1071 CETDNDDCVAHKCRHGAQCVDA-VNGYTCICPQGFSGLFCEHPPPWVLLQTSPCDQYECQ 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1130 NGAQCIVVQQEP----TCRCPPGFAGFRCEKLITV---NFVGKDSYVEL-ASAKVRPQA 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1296 DRPLGGFHGCIHEVRINNELQD--FKALPPQSLGVSPGCKSCTVCRHGLCRSVEKDSVVC 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                         159 CPT----CRDRPCONGGOCHDSESSYVCVCPAGFTGSRCEHS-----QALHCHPEACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 PDATCV---NRPDGRGYTCRCHLGRSGLRCBEGVTVTTPSLSGAGSYLALPALTNTHHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 RLDVBFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYE-LGSGLAVLRSAEPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 GRWHRVSAERLINKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSP----A
                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                                                                                                                                   Length 1523;
                                                                                                                                                                                                                                                                                Query Match
10.1%; Score 387; DB 2; Length 15
Best Local Similarity 28.6%; Pred. No. 6.7e-17;
Matches 113; Conservative 52; Mismatches 148; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 CQLREPCLHGGTCQGTR----CLCLPGFSGPRCQQ 491
                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381 TNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIG-
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A; Note: 1229-Gly and 1233-Ser were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 143-485;1279-5147 <MAH>
A;Cross-references: GB:M80537
A;Accession: B41087
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A; Residues: 1-142;487-1278 <MA2>
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                                                               A; Molecule type: mRNA
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R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, B.; Yamada, T.; Little, M.H.
R;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, B.; Yamada, T.; Little, M.H.
A;Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, B.; Yamada, T.; Little, M.H.
A;Title: Distinct but overlapping expression patterns of two vertebrate slit homologs in A;Reference number: Z22177; MUID:99279238; PMID:10349621
A;Reference number: Z22177; MUID:99279238; PMID:10349621
A;Retence number: MID: MID:99279238; PMID:10349621
A;Residues: 1-1025 - HOL>
A;Residues: 1-1025 - HOL>
A;Cross-references: EMBL:AF074960; NID:94151258; PID:94151259; PIDN:AAD04345.1
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A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: Slit2
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
                                                         1300 LYYNGLKVLNMAAENDANIAIVGNVRLVGEVPSSMTTESTÄTAMOSEMŠTSIMETTTTLA 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 NTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLA-VLRS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679 NITLQIATDED-----SGILLYKGDK-----DHIAVELYRGRVRASYDTGSHPASAIYS 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 VETINDGNFHIVELLTLDSSLSLSVDGGSPKVITNLSKQSTLNFDSPLYVGGMPGKNNVA 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEPLALGRWHRVSAERLINKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVE----P 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATC 433
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                                                                                                                                                                                                                                                                                                                                      secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
NiAlternate names: neurogenic extracellular slit protein
CiSpecies: Mus musculus (house mouse)
CiSpecies: il-Jan_2000 #sequence_revision 11-Jan-2000 #text_change 16-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEGFS protein - rat
N;Alternate names: slit protein homolog
N;Alternate names: slit protein homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C;Accession: T13953
E;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
----APDVATLTGGRFSSGITGCVKNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNGAQCIIRINEP----ICQCLPGYLGEKCEKLVSV---NFVNKESYLQIPSAKVRPQT
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                                                                                                                                                                              1360 TSTARRGKPPTKEPISOTTODILVASAECPS 1390
                                                                                                                     675 LHSARPGAPPQPLDLQHRAQAGANTRPCPS
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C;Genetics:
A;Introns: 1372/1
A;Introns: 1372/1
C;Genetics:
C;Superfamily: neurexin; EGF homology
C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; extracellu
F;1-27/Domain: signal sequence #status predicted <SIG>
F;202-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
C;Accession: A48216; B48216
R;Jebkaryov, X.A.; Seadhof, T.C.
Proc. Natl. Acad. Sci. U.S.A. 90, 6410-6414, 1993
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and A;Reference number: A48216; MUID:93342001; PMID:8341647
                                                                                                                                                                                                                                                                                                                                                                                            4333 RCGGFAGQCIDRWSSSLCQCGG-----HLQSPDCSDSLEPITLG----EGAFVEFR 4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IRHPTPLALGHP----HTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GEVVFK 443
GIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 EITLSFKTWORNGLILHTG-------KSADYVNLALKDGAVSLVINLGSGAFBA
                                                                                                                                                                                                                       4380 ISEIYRRMQLLDNLYNSKSAMLDNQQMRERRAVSNFSTASQIYEAPKMLSMLFRIYKDQG
                                                                                                                                                                                                                                                                     556 LLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSE-DPINDGEWHRVTALR
                                                                                                                                                                                                                                                                                                                                                            615 EGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATL-------TGGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 DSESSSYVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYTCRCHLGRSGLR
                                                                                                                                                                                                                                                                                                                 4440 QILY-----AATNOMFTSLSLREGRLVYYSKQHLTINMTVQETSTLNDGKWHNVSLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 BIKITERPDSADGMLLYNGOKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSG-MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 YPDYGAIPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCH
                                                                                         472 TCQGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDA--PGQYGAYFHDDGFLAFP
                                                                                                                                                                                --SLPEVPETIELEVRTSTASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 SPSTADLPGSPVSNNFMGCLKEVVYKNNDIRLELSRLARIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.0%; Score 382; DB 2; L.
Best Local Similarity 19.8%; Pred. No. 1.3e-16;
Matches 175; Conservative 138; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4531 -EAFVGCLANVTVNNEL-----QPLN 4550
                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 SSGITGCVKNLVLHSARPGAPPPQPLD 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurexin III-alpha secreted type 1 precursor
                                              GI----LAGCNROACO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
Molecule type: mRNA,
,Residues: 1-1438 <USH>
,Cross-references: GB:L14851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-1368,1372-1438
;Cross-references: GB:L14851
                                                                                                                                                                                   530 -GHVFSR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPVGTLINFNKQPLMIGGLSSADPILERPGQVHSDDLVGCLHSVHIGGRALNLS-SPLQQK 4314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SBLLÓKEVİVĠYEPCSEPÖVCENGĠVCSATMRLLD 3974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGSGMATIRHPTPLALGHFHTVTLLRSLTQGSLIVG-----DLAPVNGTSQGKFQGLD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 INE-----ELYLGG---YPDYGAIPKAGLSSGFIG--CVR-------ELRI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 QGEEIVFHDINLTAHGISHC----PTCRDRPCQNGGQCHDS-ESSSYVCVCPAGFIGSR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GLNLHTL-LYLGGVEPSVPL--SPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ITFRPDSADGMLLYNGQKRVPGSPTNL------ANRQPDFISFGLVGGRPEFRFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEHSOALHCHPEACGPDATCVN-RPDGRGYTCRCHLGRSGLRCBEGVTVTTPSLSGAGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4089 CE-SVSDSCRPNPCLHGGLCVSLKP---GYKCNCTPGRYGRHCERFSYGFQPL----SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SGLAVLRSAEPLALGRWHRVSAERLNKDGSLRV----NGGRPVLRSSPGKSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.0%; Score 383; DB 1; Length 5147; 22.9%; Pred. No. 4.7e-16; ive 97; Mismatches 265; Indels 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;4584-4609/Domain: transmembrane #status predicted <TMM>
F;4610-5147/Domain: intracellular #status predicted <INT>
  497-599/Domain: cadherin repeat homology cCR5>602-708/Domain: cadherin repeat homology cCR6>718-822/Domain: cadherin repeat homology cCR7>1318-342/Domain: cadherin repeat homology cCR9>691-942/Domain: cadherin repeat homology cCR9>
                                                                                                               1052-1153/Domain: cadherin repeat homology
1156-1278/Domain: cadherin repeat homology
1281-1384/Domain: cadherin repeat homology
11387-1489/Domain: cadherin repeat homology
1492-1601/Domain: cadherin repeat homology
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Best Local Similarity 22.94
Matches 185; Conservative
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DNSNTHSLKVDTKVVTQVINGAK-----NLDLKGDLYMAG-----LAQGMYSNLPKLVA 1014
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                                                                                                                                                                 115 YPDYGALPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561 SVNSRRTPFTAS-GESEILDLEGDMYLGGLPENRAGLILPTELWTAMLNYGYVGCIRDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GEVVFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSESSSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WGRICEREASILSYDGSMYMKVIMPMVMHTEAEDVSFRFMSQRAYGLLVATISRDSADTL
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                                                                                                                       1 EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSG-MAT
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                                                                                                                                                                                                                                           60 IRHPTPLALGHF----HTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGG
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Length 1471;
Query Match 10.0%; Score 382; DB 2; Length 14 Best Local Similarity 19.8%; Pred. No. 1.3e-16; Matches 175; Conservative 138; Mismatches 273; Indels
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Job time : 28.1076 secs
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 16-May-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
Ciscession: B48218; C48218
Cistary-1994 #sequence_revision 26-May-1994 #text_change 09-Dec-2002
Ciscession: B48218; C48218
A;Title: Neurexin IIIalpha: extensive alternative splicing generates membrane-bound and A;Reference number: A48216; MUID:93342001; PMID:8341647
A;Accession: B48218
A;Status: preliminary
A;Nolecule type: mRNA
A;Resiques: 1-1471 < USH>
A;Cross-references: GB:L14851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: neurexin; EGF homology
C;Keywords: alternative splicing; brain; cell surface component; duplication; receptor;
F;1-27/Domain: signal sequence #status predicted <SIG>
F;02-234/Domain: EGF homology <EGF>
F;651-683/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           966 DNSNTHSLKVDTKVVTQVINGAK----NLDLKGDLYMAG-----LAQGMYSNLPKLVA 1014
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                                             VRSQKNTKVDFFAVELLDGNLYLLLDMGSGTIKVKATQKKANDGSWYHVDIQRDGRSGTI 560
                                                                                                                                                                                                                                              RVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPS-----VPLSPATNMSAH-FRGCVGEVS 395
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         CEEGVIVITIPSLSGAGSYLALPALINTHHELRLDVEFKPLAPDGVLLFSGGKSGPVE--- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            852 LCKNGDIDYCELKARFGLRNIIADPVTFKTKSSYLTLATLQAYTSMHLFFQFKTTSADGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739 RLELDGGRVKLMVNLDCIRINC---NSSKGPETLY-AGQKLNDNEWHTVRVVRRGKSLKL
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A;Molecule type: mRNA
Residues: 1-1368,1372-1471 ·
A;Cross-references: GB:L14851
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March 9, 2004, 17:19:08; Search time 51.7431 Seconds (without alignments) 2876.963 Million cell updates/sec
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3825
1 BIXITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705
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Cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep: *
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Cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep: *
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ptodata/1/pubpaa/USO7_NEW FUB.pep/

ptodata/1/pubpaa/PCTUS_FUBCOMB.pep/

ptodata/1/pubpaa/USO8_NEW FUB.pep/

Ptodata/1/pubpaa/USO8A_FUBCOMB.pep/

ptodata/1/pubpaa/USO8A_FUBCOMB.pep/
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 180, App	Sequence 34, Appl	Sequence 4433, Ap	Sequence 503, App	Sequence 36, Appl	Sequence 3058, Ap	Sequence 541, App	Sequence 179, App	Sequence 102, App	Sequence 78, Appl	Sequence 102, App	Sequence 25, Appl	Sequence 26, Appl	Sequence 10, Appl	Sequence 27, Appl
, OI	US-10-094-886-180	US-10-016-283-34	US-10-108-260A-4433	US-09-866-050A-503	US-10-016-283-36	US-10-104-047-3058	US-09-764-853-541	US-09-764-898-179	US-09-764-881-102	US-10-073-865-78	US-10-242-747-102	US-10-016-283-25	US-10-016-283-26	US-09-978-249-10	US-10-016-283-27
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* Query Match Length DB	1931	1940	775	819	492	463	432	432	432	432	432	456	440	375	390
% Query Match	23.6	22.5	22.0	21.8	16.7	16.4	15.8	15.8	15.8	15.8	15.8	15.2	15.1	14.2	13.8
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Result No.	н	7	m	4	Ŋ	9	7	80	o,	10	11	12	13	14	15

Sequence 29, Appl Sequence 69, Appl Sequence 359, App Sequence 21, Appl Sequence 28, Appl Sequence 28, Appl	000000		1000000	Sequence 290, App Sequence 290, App Sequence 290, App Sequence 290, App Sequence 290, App
3-737-14 10-038-8 10-291-1 09-970-9 09-970-9	10-038-854-6 10-297-639-2 10-289-776-2 39-766-511B- 10-189-123-6 10-188-495-6	10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10-038-10	10-174-590-2 10-174-590-2 10-175-737-2 10-173-706-2 10-175-738-2	999999
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## **ALIGNMENTS**

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APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
                                                                                                                                                                                                                                    Malyankar, Uriel M.
Boldog, Ferenc
Guo, Xiaojia
Shenoy, Suresh
Padigaru, Muralidhara
Taupier, Raymond J., Jr.
           Application US/10094886
... US20040002120A1
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Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
                                                                       APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A.
                                                                                                                                                                                                                                                                                                                                                                                            Pena, Carol
Gangolli, Esha
Gusev, Vladimir
Smithson, Glennda
Zerhusen, Bryan
                                                                                                                                               Patturajan, Meera
Burgess, Catherine
Vernet, Corine A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerlach, Valerie
Pochart, Pascal
                                                                                                                                                                                                                                                                                                                                                                                Stacie
                                                                                                                                                                                                                      Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                              Casman,
US-10-094-886-180
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1336 SLVPVEPGRWHRLELSRHWRQGTLSVDGETPVVGESPSGTDGLNLDTNLYVGGIPEEQVA 1395
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                       556 ILLWOGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALRE
                                                             616 GRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITGCVKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REPERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/10/016,283
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US/09/077,955A
PRIOR PILING DATE: 1996-09-10
PRIOR PILING DATE: 1996-12-13
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                                                                                                                                                                                                                                                                              674 VLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/10016283 Publication No. US20020164702A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 32.09
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Rattus
US-10-016-283-34
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US-10-016-283-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 GOCHDSESSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1448 APCONLEAGREHCOCPPGRVGPTCADEKS-PCQPNPCHGAAPCRVLPEG-CAQCECPLGR
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PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR PRILING DATE: 2001-06-17

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/218,510

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/214,281

PRIOR APPLICATION NUMBER: 60/274,194

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-09

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ORGANISM: Homo sapiens
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Matches 242; (
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CY 464 REPCIHGGTCGGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFH 521  Db 583LHCQKAIIEAIEIPQFIG	609 PDILKRVSGSRSNVFMRFKTTAKDGLLLWRGDSPMRPNSDFISLGLRDG 582 HLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVN [	RESULT 4  RESULT 4  US-09-866-050A-503  Sequence 503, Application US/09866050A  Publication No. US20030040471A1  Sequence 503, Application US/09866050A  Publication No. US20030040471A1  APPLICANT: Watson, James D.  APPLICANT: Strachan, Lorna  APPLICANT: Winnble, Rene  APPLICANT: Winnble, Rene  APPLICANT: Winnble, Krishanand D.  TITLE OF INVENTION: Compositions Isolated From Skin Cells  TITLE OF INVENTION: Compositions Isolated From Skin Cells  TITLE OF INVENTION: Compositions Isolated From Skin Cells  TITLE OF INVENTION: And Methods for Their Use  FILE REFERENCE: 11000.1011c4U  CURRENT APPLICATION NUMBER: US/09/866,050A  CURRENT FILING DATE: 2001-05-24  NUMBER OF SEQ ID NOS: 725  SOFTWARE: PastSEQ for Windows Version 4.0  SEROID NO 503  LENGTH: 819  TYPE: PRT  COGANTH: 819	Decription   21.8%;   Score 832;   DB 10;   Length 819;     Best Local Similarity   29.3%;   Pred, No. 2.66-59;     Matches   210;   Conservative   109;   Mismatches   264;   Indels   134;   Gaps   17;
Db 1717VEKSVG 1757  CY 510 NDAPGQYGAYFHDDGFLAFPGHVFSRSLPFVFTTELEVRTSTASGILLWQG 561  Db 1758DLETLAFDGRIYIEVLAVIESEKALQSNHFELSLRTEARGGILLWG	н Д ж г	RESULT 3   US - 108 - 260A - 4433   US - 108 - 108 - 260A - 4433   US - 108 - 108 - 260A - 4433   US - 108 - 108 - 260A - 4433   US - 108 - 108 - 260A - 4433   US - 108 - 260A - 4433   US - 108 - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A - 260A -	RHPTPLALGHEHTVTLLRSLTQGSLIVODLAPVNGTSQCKFQGLDLNEELYLGGGYDD-VG

Db 279VCLCPGGFSGPHCEKGL	RESULT 6  US-10-104-047-3058  US-10-104-047-3058  Sequence 3058, Application US/10104047  Publication No. US2003023639241  GENERAL INFORMATION:  APPLICANT: HELIX RESEARCH INSTITUTE  TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA  FILE REFERENCE: H1-A0105  CURRENT APPLICATION NUMBER: US/10/104,047  PRIOR FILING DATE: 2002-03-25  PRIOR FILING DATE: 2002-03-25  NUMBER OF SEQ ID NOS: 4096  SOFTWARE: Patentin Ver. 2.1  SEQ ID NO 3058  LENGTH: 463  TYPE: PRI  CORGANISM: HOME Sapiens  US-10-104-047-3058	Query Match   16.4%;   Score 628;   DB 15;   Length 463;     Best Local Similarity 28.7%;   Pred. No. 6.4e-43;     Matches 162;   Conservative 80;   Mismatches 198;   Indels 124;   Gaps 16;     Qy	OY 209 PDATCVNRPDGRGYTCRCHLGRSGLRCEEGUTVTTPSL-SGAGSYLALPALTNTHHEL 265  DD 51	QY         322 LALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPT 381                     :     :     :     :     :     :     :     :     :     :     :       :     :     :     :     :     :     :     :     :     :     :     :       :     :     :	QY 442 QCLCRDGFKGDLCEHERNPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIAE 499 Db 261 DCDCPLGFFG	
OY 347 RPULRSSPGKSQGINLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYS 406  525 KVVEGMAEGGFTQİKCNTDİFİLİ	DD 707 YNLGSGVASIMVNGSFSDGRWHENVRANDGGSGKITVDDYGARTGGKSPGWARGIANINGAL 766  QY 647 YNGGABDVATLIGGRESSGTTGCVRULVLHSARPGAPPOPLDLQHRAQAGANTRPC 703  [1] ::   :   :     :	; PRIOR FILING DATE: 1996-12-13 ; NUMBER OF SEG 10.05: 36 ; SOFTWARE: Patentin Ver. 2.0 ; SEG 1D NO 36 ; TYPE: PRT 7 ; TYPE: PRT 7 ; ORGANISM: Homo sapiens US-10-016-283-36	Query Match 16.7%; Score 640.5; DB 13; Length 492; Best Local Similarity 33.0%; Pred. No. 6.6e-44; Matches 183; Conservative 59; Mismatches 173; Indels 139; Gaps 18; QY 202 CHPBACGPDATCWINPDGRGYTCRCHIGRSGIRCEGGYTVTTPSLSGAGSYLALPALTNT 261	Qy         262 HHELRLDVEFYPLAPDGYLLFSGGKSGPVEDFYSLAWVGGHLEFRY 307           bb	Oy 363 HTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQG 412	

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384 KITVDDYGARTGKSPGWARQLNINGALYVGGMKEIALHTNRQYMRGLVGCISHFTLST-- 441
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                                                          620 SIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSAR
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15.8%; Score 605; DB 9; Length 432;
Best Local Similarity 29.0%; Pred. No. 4.5e-41;
Matches 157; Conservative 75; Mismatches 188; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ206
FURRENT APPLICAN NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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Patent No. US20020090672A1
GENERAL INFORMATION:
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US-09-764-853-541
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LENGTH: 432
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231 SGLRCEEGVIVITPSL-SGAGSYLALPALTNITHHEL---RLDVEFKPLAPDGVLLFS--- 283
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15.8%; Score 605; DB 9; Length 432;
Best Local Similarity 29.0%; Pred. No. 4.5e-41;
Matches 157; Conservative 75; Mismatches 188; Indels 122; Gaps
                       GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PZ201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 179
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Sequence 179, Application US/09764898
Patent No. US20020090673A1
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US-09-764-898-179
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-073-865-78
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US-10-242-747-102
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Best Local Similarity 29.0%; Pred. No. 4.5e-41;
Matches 157; Conservative 75; Mismatches 188; Indels 122; Gaps
                                                                        file wrapper
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapp NUMBER OF SEQ ID NOS: 192
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 432
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TITLE OF INVENTION: Nucleic Acids, Froteins, and Antibodies
FILE REFERENCE: 9250921
CURRENT APPLICATION NUMBER: US/10/073,865
CURRENT APPLICATION NUMBER: US/10/073,865
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 78
LENGTH: 432
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Publication No. US20030044904A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-764-881-102
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Query Match
15.8%; Score 605; DB 14; Length 432;
Best Local Similarity 29.0%; Pred. No. 4.5e-41;
Matches 157; Conservative 75; Mismatches 188; Indels 122;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ07C1
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,881
PRIOR APPLICATION NUMBER: 06/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-28
PRIOR PRIING DATE: 2000-07-11
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PRIOR FILING DATE: 2000-07-14
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Publication No. US20040005577A1
GENERAL INFORMATION:
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Best Local Similarity 29.0%; Pred. No. 4.5e-41;
Matches 157; Conservative 75; Mismatches 188; Indels 122; Gaps
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              PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR PILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 102
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Sequence 25, Application US/10016283
Publication No. US20020164702A1
GENERAL INFORMATION:
APPLICANT: Valentuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TITLE OF INVENTION: NOVEL TYROSINE KINASE
CURRENT APPLICATION NUMBER: US/10/016,283
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US/09/077,955A
PRIOR APPLICATION NUMBER: PCT/US96/20696
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APPLICATION NUMBER: 60/217,496
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; ORGANISM: Homo sapiens
US-10-242-747-102
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                                                                                                                                                                                                                                                                                                                                                                         25 TASGODGSGPFIA-DFNGFSHLELRGLHTFARDLGEKMALEVVFLARGPSGLLLYNGOKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 DGKGDFVSLALRDRRLEFRYDLGKGAAVIRSREPVTLGAWTRVSLERNGRKGALRVGDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 RVLGESP-KSRKVPHTVLNLKEPLYVGGAPDFSKLARAAAVSSGFDGAIQLVSLGGRQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------DVDTLAFDGRTFVEYLNAVTESELANEIPVEKALOSNHFELSLRTEAT
                                                                                                                                                                                                                                                                                                                                           --LDVEFKPLAPDGVLLFSGGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                          288 GPVEDFVSLAMVGGHLEFRYELGSGLAVIRSAEPLALGRWHRVSAERLNKDGSLRVNGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DLTYSFLGSQGIGQCYDSSPCER---QPCQHGATCMPAGEYEFQCLCRDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------REAAY-----VCLCPGGFSGPHCEKGL------VEXSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 SGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 PVLRSSPGKSQG----LNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450 KGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGG
                                                                                                                                                                                                                                                                                       Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Valentuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REPERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/10/016,283
CURRENT APPLICATION NUMBER: US/09/077,955A
PRIOR PILING DATE: 1998-10-10
PRIOR PLILING DATE: 1998-10-10
PRIOR PLILING DATE: 1998-10-10
PRIOR PLILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTI NOS: 2.0
SEQ ID NO 26
LENGTH: 440
TYPE: PRT
                                                                                                                                                                                                                                        DB 13; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 TPEHVLROVDVT-SPAG------HPCTRASGHPCLNGASCVP
                                                                                                                                                                                                                                   Query Match 15.2%; Score 579.5; DB 13; Best Local Similarity 32.7%; Pred. No. 6e-39; Matches. 168; Conservative 57; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 705
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DVVVGR------HPLHLLEDAVTKPELRPCPT 455
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                                                                                                                                                                                                                                                                                                                                        242 TIPSLSGAGSYLALPALTNIHHELR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/10016283
Publication No. US20020164702A1
GENERAL INFORMATION:
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-10-016-283-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-016-283-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-016-283-26
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Qy 382 NMSAHFRGCVGEVSYNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQEGATCMPAGEYEF 441  bb 116 GVLKDPRSGSIOKIILNDRTIHVKHDFTSGVNVENAAHPCVRAACAGGSCRPKKE-GY 172  Qy 442 QCLCRDGFKGDLCEHEENPCQLREPCLHGGTCGTRCLCLPGFSGPRCQQGSGHGIAE 499  Db 173 DCDCFLGFEGLHCQKALIEATENPQFIG	201		CURRENT APPLICATION WOMBER: US/10/016,283	Query Match Best Local Similarity 33.0%; Pred. No. 8.18-35; Matches 149; Conservative 50; Mismatches 134; Indels 118; Gaps 14;  Qy 291 EDFVSLAMVGGHLERRYELGSGLAVLRSAEPLAGRWHRVSAERLNKDGSLRVNGGRPVL 350	Oy 351 RSSPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRL 401  B1 GESP-KSRKVPHTVLNLKEPLYVGGAPDFSKLARAAAVSGFDGAIQLVSLGGRQLLTPE 139  Qy 402DLTYSFLGSQGIGQCYDSSPCEROPCQHGATCMPAGEYEFQCLCRDGFKGD 452	453 LCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQSGHGIAESDWHLEGSGGNDA  453 LCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQSGHGIAESDWHLEGSGGNDA  172
Best Local Similarity 32.9%;   Pred. No. 1.1e-38;   Matches 163;   Conservative 55;   Mismatches 145;   Indels 132;   Gaps 15;   Qy 261   THHELR	SFLGSQ 41 SFAG 20 LREPCL 46 - REAAY 22 OGFLAF 52	529 PGHVPS 529 PGHVPS 257 DGRTPV 573 FISIGH 573 FISIGH 573 YVALAI 633 SPGPNV 7373 SPLGAT	Oy 691 QHRACAGANTRECES 705  Db 425 LEDAVTKPELRPCFF 439  RESULT 14  US-09-978-249-10  ; Sequence 10, Application US/09978249  ; Sequence 10, Application US/09978249  ; Patent No. US20020106780A1  ; APPLICANT: Fiscella, et al.  ; TITLE OF INVENTION: Extracellular Matrix Polynucleotides, Polypeptides, and Antibodie	CURRENT PILING DATE: 2001-10-17 CURRENT FILING DATE: 2001-10-17 PRIOR APPLICATION NUMBER: PCT/USO1/11643 PRIOR FILING DATE: 2001-04-11 PRIOR FILING DATE: 2000-04-11 PRIOR PILING DATE: 2000-04-18 NUMBER: PCT/USO1/10-12	Score 543 6. DR 9. Length	Destruction Similarity 30.6%; Score 343.5; Destruction 375; Best Local Similarity 30.6%; Procedure 161; Indels 77; Gaps 12; Matches 136; Conservative 70; Mismatches 161; Indels 77; Gaps 12; Conservative 70; Mismatches 161; Indels 77; Gaps 12; Cy 265 IRIDVEFFEDGVLLFSGEKSGPVEDEVSLAWVGGHLEFFFEDGSGLAVLRSAEP 321  Db 1 MEFEITFRPDSGDGVLLYSYDTGSKDFLSINLAGGHVEFFFCGSGTGVLRSEDP 55  Qy 322 LALGRWHRVSAERLNKDGSLRVNGGRPVLRSSPGKSGGLALHTLLYLGGVEPSVFLSPAT 381

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<sup>507</sup> REGSLLVGNEARVIGSSPLGATQLDIDGALMLGGLFELFVGFALLFKAYGTGF 675 LHSARPGAPFPQPLDLQHRAQAGANTRPCPS 705

<sup>367</sup> VGR-----HPLHLLEDAVTKPELRPCPT 389

Search completed: March 9, 2004, 17:25:14 Job time : 54.7431 secs

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence 2, A Sequence 16, Sequence 19, Sequence 19, Sequence 1, A Sequence 1, A Sequence 5, A

Sequence 30, Sequence 2, A Sequence 2, A

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Sequence 30, Application US/08644271

Sequence 30, Application US/08644271

Patent No. 5814478

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS

TITLE OF INVENTION: AND LIGANDS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: TAILYOWN

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: BARDABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BARDABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BARDABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: 184500 Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/644,271

FILING DATE: 10-MAY-1996

CLASSIFCATION NUMBER: US/08/657

FILING DATE: 115-DEC-1995

ATTORNEY/AGENT INFORMATION:

TELEFORMATION: A35

REFERENCE/DOCKET NUMBER: REG 195A

TELEFAX: 914-345-7721

TELEFAX: 914-345-7721
                                             US-09-540-153-9

US-09-562-702A-12

US-09-562-702A-12

US-09-077-955-29

US-09-11-647-7

US-09-540-153-7

US-09-540-153-7

US-09-540-153-7

US-08-185-42-16

US-08-185-42-16

US-08-185-43-19

US-08-185-43-19

US-08-185-32-34-19

US-08-93-23-34-19
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US-09-077-955-30
US-09-911-842A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALI GNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1940 amino acids
                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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LOCATION: 1:..1940
CTHER INFORMATION:
US-08-644-271-30
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3825
1 EIKITFRPDSADGMLLYNGQ......QPLDLQHRAQAGANTRPCPS 705
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Sequence 3
Sequence 3
Sequence 2
Sequence 2
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Sequence 2
Sequence 2
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Patent No.
Sequence 2
Sequence 8
Sequence 8
Sequence 4
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/ cgm2_6/ptodata/2/laa/5A_COMB.pep:*
/ cgm2_6/ptodata/2/laa/5B_COMB.pep:*
/ cgm2_6/ptodata/2/laa/6A_COMB.pep:*
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/ cgm2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/ cgm2_6/ptodata/2/laa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-540-153-2
US-09-312-283C-183
US-09-312-283C-183
US-09-182-024A-2
US-08-460-309-5
US-08-460-309-5
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US-09-077-955-25
US-09-077-955-26
US-09-077-955-27
US-09-077-955-27
US-09-188-930-183
US-09-191-647-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match 1
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Perfect score:
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Matches 239;
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                                                Gaps
                                             Indels 135;
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
TILE REPERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER FILING DATE: 1996-12-13
EARLIER FILING DATE: 1996-05-10
EARLIER PILING DATE: 1996-05-10
EARLIER RILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
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                     Pred. No. 7.4e-64;
; Mismatches 280;
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Patent No. 6413740
GENERAL INFORMATION:
32.0%; Pic.
                  Best Local Similarity 32.04
Matches 239; Conservative
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US-09-077-955-34
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                                                                                                                                                                                                                                             1627 GALQVGDGPRVLGESP-KSRKVPHTMLNLKEPLYIGGAPDFSKLARGAAVSSGFSGVIQL 1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278
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                                                                                                                                                                                                                                                                                                                                                    1456 QALEAGMFLCOCPPGRFGPTCADEKS-PCOPNPCHGAAPCRVLSSG-GAKCECPLGRSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCEEGVIVITIPSLSGAG----SYLALPALINTHHEL----RLDVEFKPLAPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLRVNGGRPVLRSSPGKSQG----LINLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------LGNPCLNGGSCVPREATYECLCPGGFSGLHCEKGL------VEKSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 CEHEENPCQLREPCLHGGTC---QGT-RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 NDAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPET-----IELEVRISTASGLLLWQG
                                                                                                       2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR
                                                                                                                                                                                                                                                                                                                                                                                                                       174 HDSESSSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSVNGKRLDLTYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDL
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                                                                                                                                                                                                              HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYG--
                                                                                                                                                                                                                                                                                                                  120 -AIPKAGLSSGFIGCVRELRIQGEEIVFHDLNLTA---HGISHC--PTCRDRPCONGGOC
22.5%; Score 862.5; DB 4; Length 1940; 32.0%; Pred. No. 7.4e-64; Live 92; Mismatches 280; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1686 VSLRGHQL----LTQEHVLRAVDVSPFADHPCTQA-----
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US-08-644-271-32
Sequence 32, Application US/08644271
Patent No. 5814478
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS; TITLE OF INVENTION: AND LIGANDS
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ROLHLLEDAVTKPELRPCPT 1939
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                                                    Conservative
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634 PGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQ 691
                                                                                                                                                                                         :: | ::::| | : | | | 426 PLGATQIDTDGALWIGGLEPVGPALPKAYGTGFVGCLRDVVVGR------HPLHIL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPALTNT 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 GHVFSRSLPEVPET------IELEVRISTASGLLIWQGVEVGEAGQGKDF 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574 ISLGLODGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRS 633
                                              366 VALAIVDGHLQLSYNLGSQPVVLRSTVÞVNTNRWLRVVAHREQREGSLQVGNEAPVTGSS
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Sequence 36, Application US/09077955A

Patent No. 6413740

GENERAL INFORMATION:
APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A

CURRENT FILING DATE: 1998-09-10

EARLIER APPLICATION NUMBER: 08/644,271

EARLIER PILING DATE: 1996-01-10

EARLIER APPLICATION NUMBER: 60/008,657

EARLIER PILING DATE: 1996-05-10

EARLIER PILING DATE: 1995-12-15

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Ver. 2.0
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16.7%; Score 640.5; DB 4;
Best Local Similarity 33.0%; Pred. No. 6.6e-46;
Matches 183; Conservative 59; Mismatches 173;
                                                                                                                                                                                                                                                                                          692 HRAQAGANTRPCPS 705
                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-955-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 CQPNPCHGAAPCRVLPEG-GAQCECPLGREGTFCQ----TASGQDGSGPFLA-DFNGFS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 16.7%; Score 640.5; DB 2; Length 492; Best Local Similarity 33.0%; Pred. No. 6.6e-46; Matches 183; Conservative 59; Mismatches 173; Indels 139; Gaps
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                           : Regeneron Pharmaceuticals, Inc. 777 Old Saw Mill Road
                                                                                                                                                                                                                                                                                                                                                                               SCPENAIRS SIGLAGE OF SERVING SOFTWARE:
SCRINGER APPLICATION DATA:
PILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTONNEY, AGENT INFORMATION:
NAME: CODERT, ROBERT UNSURES: 36,108
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
REFERENCE/DOCKET NUMBER: 36,108
TELECHONE: 914-345-7400
                                                                                                        STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TYPE: IBM Compatible
TYPE: IBM Compatible
TYPE: IBM COMPATIBLE
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SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
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LOCATION: 1...492

JOCHER INFORMATION:

US-08-644-271.32
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CORRESPONDENCE ADDRESS
                                          STREET: ///
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529 PGHVFSRSLPEVPET------
                                            Sequence 26, Application US/09077955A
Patent No. 6413740
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                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-077-955-26
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                               US-09-077-955-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 ------DVDTLAFDGRTFVEYLNAVTESELANEIPVEKALQSNHFELSLRTEAT 313
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634 PGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQ 691
                               --HPLHLL 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 PVLRSSPGKSQG----LINLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRL-
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                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS FILE REFERENCE: REG195-B-FCT-US
FILE REFERENCE: REG195-B-FCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1996-10-10
EARLIER APPLICATION NUMBER: 06/644,271
EARLIER APPLICATION NUMBER: 06/644,271
EARLIER APPLICATION NUMBER: 06/610
EARLIER APPLICATION NUMBER: 06/008,657
EARLIER APPLICATION NUMBER: 60/008,657
SARLIER PILING DATE: 1995-12-15
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SSETURNE APPLICATION NUMBER: 06/008,657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.2%; Score 579.5; DB 4; Length 456; Best Local Similarity 32.7%; Pred. No. 8.8e-41; Matches 168; Conservative 57; Mismatches 156; Indels 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 TPEHVLRQVDVT-SFAG------HPCTRASGHPCLNGASCVP
                  | :::|| |:::|| 426 | BIGATQLDTDGALWLGGLPELPVGPALPKAYGTGFVGCLRDVVVGR
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Patent No. 6413740
                                                                    592 HRAQAGANTRPCPS 705
                                                                                                   478 EDAVTKPELRÞÓÞT 491
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US-09-077-955-25
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261 THHELR-------LDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFR 306
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GAPPLICANT: Valenzuela et al., David M.
APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILLE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER PELLING DATE: 1996-12-13
EARLIER PILING DATE: 1996-12-13
EARLIER PILING DATE: 1996-12-13
EARLIER PILING DATE: 1996-12-13
SARLIER PILING DATE: 1996-12-15
NUMBER: OF SEQ ID NOS: 36
SOFTWARE: PATENT NOVE: 2.0
SEQ ID NO 26
IENGTH: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.1%; Score 576; DB 4; Length 440;
Best Local Similarity 32.9%; Pred. No. 1.6e-40;
Matches 163; Conservative 55; Mismatches 145; Indels 132;
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Patent No. 6413740
GENERAL INFORMATION:
APPLICANT: VARIATION:
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRL
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411

361

226 528 256 572

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648 LCDE-----GEDLFNPLPGDQVQAR----
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APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Ensee, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/191,647
CURRENT APPLICATION NUMBER: 60/065,544
EARLIER APPLICATION NUMBER: 60/065,544
EARLIER PILING DATE: 1998-11-14
EARLIER PILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                      Indels
                                                                                                                                                                      Query Match 10.4%; Score 397.5; DB 3; Best Local Similarity 27.6%; Pred. No. 5e-25; Matches 145; Conservative 64; Mismatches 185;
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Patent No. 6046015
GENERAL INFORMATION:
              ; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (717)...(717)
US-09-188-930-183
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; ORGANISM: human
US-09-191-647-2
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LENGTH: 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DDKVSLALRDRRLEFRYDLGKGAAVIRSREPVTLGAWTRVSLERNGRKGALRVGDGPRVL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.8%; Score 528; DB 4; Length 390;
Best Local Similarity 33.0%; Pred. No. 1.6e-36;
Matches 149; Conservative 50; Mismatches 134; Indels 118;
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steman, Matthew
APPLICANT: Ornaus, Rene
APPLICANT: Onnus, Rene
APPLICANT: Onnus, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOUTHARE: FeatSEQ for Windows Version 3.0
SEQ ID NO 183
LENGTH: 771
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FILE REFERENCE: REG195-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 60/008,657
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1995-12-15
NUMBER: 0F SEQ ID NOS: 36
SEQ ID NO 27
LENGTHARE: PATENTIN VET. 2.0
SEQ ID NO 27
LENGTHIS SAG ID NOS: 36
SEQ ID NO 27
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Patent No. 6150502
                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens US-09-077-955-27
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158 HC----PTCRDRPCONGGOCHDSESSYVCYCPAGFTGSRCEHSQAL-----HCHPEAC 207
                                          374 QNGAQCIIRVNEP----ICQCLPGYLGEKCEKLVSVSI--LVNKESYLQIPSAKVRPQT 426
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                                                                                                                        208 GPDATC---VNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPAL----T
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                                       57; Gaps
                                                                          158 HC----PICRDRPCQNGGQCHDSESSYVCVCPAGFIGSRCEHSQAL----HCHPEAC
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   DB 3; Length 1525;
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APPLICANT: Goodman, Corey
APPLICANT: Brose, Katja
APPLICANT: Brose, Katja
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REPRENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIOR PILING DATE: 1997-11-14
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOOTWARR: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.4%; Score 397.5; DB 3; Length Best Local Similarity 29.7%; Pred. No. 1.3e-24; Matches 108; Conservative 58; Mismatches 141; Indels
                                       Indels
Query Match
10.4%; Score 397.5; DB 3;
Best Local Similarity 29.7%; Pred. No. 1.3e-24;
Matches 108; Conservative 58; Mismatches 141;
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; ORGANISM: human
US-09-540-245A-2
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319 AEPLALGRWHRVSAERLINKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVE----P 373
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APPLICANT: Goodman, Corey
APPLICANT: Goodman, Corey
APPLICANT: Bross, Katja
APPLICANT: Bross, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-33;
CURRENT APPLICATION NUMBER: US/09/540,153
CURRENT FILING DATE: 2000-03-31
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
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Best Local Similarity 29.7%; Pred. No. 1.3e-24;
Matches 108; Conservative 58; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09540153 Patent No. 6270995
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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; ORGANISM: human
US-09-540-153-2
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GENERAL INCOMPANION:
CHARACTURY: Connolly, Timothy
APPLICANT: Rajput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
FILE REFERENCE: 64010-271
CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT APPLICATION NUMBER: 60/063,946
FRIOR APPLICATION NUMBER: 60/063,946
FRIOR FILING DATE: 1998-10-31
FRIOR FILING DATE: 1998-10-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2
LENGTH: 1523
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                                                                                                                                                                                                                                                       10.3%; Score 394; DB 4; L 28.3%; Pred. No. 8.8e-25; ive 59; Mismatches 160;
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FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 183
LENGTH: 716
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Matches 126; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                 TYPE: PRT
ORGANISM: Mouse
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: Compositions for Their Use
TITLE OF LINVENTION: and Methods for Their Use
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
SOFFER OF SEQ ID NOS: 425
NUMBER OF SEQ ID NOS: 425
SOFFER OF SEQ ID NOS: 425
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Patent No. 6573055
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ontse, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Rene
APPLICANT: Kumble, Rene
APPLICANT: Murison, James G.
TITLE OF INVENTION: and Methods for Their Use
                                                                                                           Sequence 396, Application US/09312283C Patent No. 6573095
1401 LCDE 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-396
                                                                                          US-09-312-283C-396
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LENGTH: 1529
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Length 1523;

BORE   LOCAL   SIGNIAL STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE   STATE
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qq	191 RTEATQGLVLWSGKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWL 246	246
Š	VDGEELVSGRSPGP	999
QQ	247 RVVAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALWLGGLPELPVGPALPKAYGTGF 306	306
δλ	667 TGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 705	
Ωp	307 VGCLRDVVVGRHPLHLLEDAVTKPELRPCPT 337	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:11:22; Search time 85.8465 Seconds (without alignments) 2320.373 Million cell updates/sec

Title: Perfect score:

US-10-006-011A-3 3825 1 EIKITFRPDSADGWLLYNGQ......QPLDLQHRAQAGANTRPCPS 705 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* Database :

geneseq11980s:\* geneseq11990s:\* geneseq2011s:\* geneseq2011s:\* geneseq2012s:\* geneseq2013s:\* geneseq2013s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aae34390 Human per	Amino	Novel	Amino		Novel	Novel	Human	Human	Rat Dr		Abb61948 Drosophil			Human		Novel	Human	Human	Aau19905 Novel hum		Human	Human	Drosop	_
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AAU07421	ADE54405	ADE54409	AAU28190	AAM78871	AAM79855	AAX27141	AAW96706	AAY04138	AAW46966	AAY27144	AAW96707	AAY04139	ADE54473	ADD49063	AAE17600	AAY27142	AAW96701	AAY17499	ADB85322
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543.5	441	441	420.5	412.5	412	407	407	407	407	407	407	407	407	401.5	398	397.5	397.5	397.5	397.5
56	27	28	53	30	31	35	33	34	32	36	37	38	6 E	40	41	42	43	44	45

## ALIGNMENTS

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An assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis comprising detecting an isomerized or optically inverted protein in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an assay for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The assay involves measuring (in a biological sample) the amount or presence of an isomerised or optically inverted protein or one or more isomerised or optically inverted from proteins such as perlecan, biglycan, decorun, fibrillin-1 or protocadherin. The assay is useful for the diagnosis or assessment of the severity of osteoarthritis or rheumatoid arthritis. The present sequence is human perlecan protein
                                                                                                                                                             Human; diagnosis; osteoarthritis; rheumatoid arthritis; perlecan.
                                                                                                                                                                                                                                                                                                                                                                                          Cloos PAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 46-67; 106pp; English.
                             AAE34390 standard; protein; 4391 AA.
                                                                                                                                                                                                                                                                                                                                                         (OSTE-) OSTEOMETER BIO TECH AS.
                                                                                                                                                                                                                                                                                                                          23-MAY-2001; 2001GB-00012626.
                                                                                                                                                                                                                                                                                            22-MAY-2002; 2002WO-EP005612.
                                                                                                                                                                                                                                                                                                                                                                                          Christgau S, Henriksen DB,
                                                                                             14-MAY-2003 (first entry)
                                                                                                                              Human perlecan protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-140389/13.
                                                                                                                                                                                                                           WO200295415-A2.
                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                            28-NOV-2002.
                                                              AAE34390;
RESULT 1
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Length 4391; 0; Indels Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-233;
Matches 705; Conservative 0; Mismatches 0; Sequence 4391 AA;

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us-10-006-011a-3.rag

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The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymolectide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the genglioside GMZ activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immine disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, proprecion and treatment of multiple sclerosis (in its various forms and passes). They may also be useful in cases of e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid polyarthritis and lupus erythematosus, including use as vaccines and in polyarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisenses sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
                                                                                                                                           Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 BIKITFRPDSADGMLLYNGOKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                                                                           Claim 1; Page 138-152; 209pp; French
                                              (INMR ) BIOMERIEUX STELHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.6
Matches 702; Conservative
                                                                                                              WPI; 2001-159475/16.
                                                                             Roecklin D, Kolbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4393 AA;
                 15-JUL-1999;
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EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                   RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA
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Amino acid sequence of a human protein.

15-MAY-2001

AAB31889

AAB31889 standard;

RESULT 2

17-JUL-2000; 2000WO-FR002057

25-JAN-2001

Homo sapiens

300

4108

3748

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Indels

Score 3815; DB 4; Pred. No. 1.1e-232; 2; Mismatches 1;

99.7%;

Length 4393;

180

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Sequence 4436 AA;

4348

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recention (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed gene therapy techniques to restore normal activity of (II) be useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant procein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the way way and the compact of the printed specification, but was obtained in the way and the compact of the printed specification, but was obtained in the way and sequences.
                        PETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSED 600
                                                                                               PINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSIYIGGAPDVATLIGG
                                                                               I OVDGEELVSGRSPGPNVAVNAKGSVY I GGAPDVATLTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                         661 RFSSGITGCVKNLVLHSARPGAPPOPLDLOHRAQAGANTRPCPS 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 53624; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #23256.
                                                                                                                                                                                                                                                                                    ABG23265 standard; protein; 4436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS87452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens,
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                                                                                                             4289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4262 PETIBLEVRISTASGLLLMQGVEVGEAGQGKDFISLGLQDGHLVFSSYFLGLDDCRYQLG 4321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; perlecan, retinol-binding plasma protein; calgranulin B; vaccine, ganglioside GWZ activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.
                                                                                                                                                                     3842 IPRAGLSSGFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSESSS
                                                                                                         3722 EIKITFRPDSADGMLLYNGOKRVPGSPTNLANROPDFISFGLVGGRPFFRFDAGSGMATI
                                                                                                                                                                                                                                                                                                                                                                241 VITPSLSGAGSYLALPALINIHHELRLDVEPKPLAPDGVLLFSGGKSGPVEDFVSLAMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4082 NIHTILYIGGVEPSVPLSPATNMGAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4142 PCERQPCQHGATCMPAGEYBFQCLCRDGFKGDLCEHBENPCQLREPCLHGGTCQGTRCLC
                                                                       1 EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                              61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPDYGA
                                                                                                                                                                                                                   121 IPKAGLSSGFIGCVRELRIQGEEIVFHDINLTAHGISHCPTCRDRPCQNGGQCHDSESSS
                                                                                                                                                                                                                                                                                         181 YVCVCPAGFIGSRCEHSQALHCHPEACGPDATCVNRPDGRGYICRCHLGRSGLRCEEGVT
                                                                                                                                                                                                                                                                                                                             3902 YVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYICRCHLGRSGLRCEEGVT
                                                                                                                                                                                                                                                                                                                                                                                                   3962 VITPSLSGAGSYLALPALINTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDLTYSFLGSQGIGQCYDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCEROPCOHGATCMPAGEYERCLCRDGFKGDLCEHEENPCOLREPCLHGGTCQGTRCLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 PETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVF-----RYQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GHLEFRYELGSGLAVIRSAEPLALGRWHRVSAERLNKDGSLRVNGGRPVIRSSPGKSOGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 LPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4322 SGEARLVSEDPFNDGEWHRVTALREGRRGSIQVDGEELVSGRSPGFNVAVNAKGSVYIGG
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4382 APDVATLTGGRFSSGITGCVKNIVLHSARPGAPPPQPLDLQHRAQAGANTRPCP 4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the C-terminal of the human perlecan protein.
                                          10;
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Query Match 99.2%; Score 3795; DB 4; Length 4436; Best Local Similarity 98.2%; Pred. No. 2.1e-231; Matches 701; Conservative 1; Mismatches 2; Indels 10
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WO200279398-A2.

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The present sequence represents a human polypeptide, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymorleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or saposin B protein the ganglioside GMZ activator, calgranulin B or saposin B protein camples. The method is used for describing or treating a degenerative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, proprosition and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis, rheumatcid polyperthritis and lugus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisenses sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KDFISLGLQDGHLVFRYQLGSGBARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQPLDL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DAPGQYGAYFHDDGFLAFFGHVFSRSLPEVPETIELEVRTSTASGLLLMQGVEVGREAGQG
                                                                                                                                                                                                                                                                                         Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 DAPGOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRISTASGLLLWQGVEVGEAGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    631 GRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGIIGCVKNLVLHSARPGAPPPQPLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                  Perron H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.9%; Score 1030; DB 4; Length 195; Best Local Similarity 100.0%; Pred. No. 1.3e-57; Matches 195; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                    Santoro L,
                                                                                                                                                                                                  Malcus C,
                                                                                                                                                                                                                                                                                                                                                                     Claim 1, Page 152-153; 209pp; French.
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                                                                                                                                                                                              Charles M,
                                                                            17-JUL-2000; 2000WO-FR002057
                                                                                                                   99FR-00009372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     691 OHRAQAGANTRPCPS 705
                                                                                                                                                       (INMR ) BIOMERIEUX STELHYS
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                                                                                                                                                                                            Roecklin D, Kolbe H,
                                                                                                                                                                                                                                   WPI; 2001-159475/16.
N-PSDB; AAF54728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 195 AA;
  WO200105422-A2
                                                                                                                 15-JUL-1999;
                                       25-JAN-2001
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SXXXXXXXXXX
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Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.

Homo sapiens

Human GPCR related protein NOV40a.

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NOVX polypeptides and polynuclectides, useful for treating a syndrome related to a human disease associated with the NOVX polypeptide e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOVI-NOV44), variants of these
                                                                                                                                                                                                                                                                                                                                                                                                                      Kekuda R, Tchernev VT, Liu X, Spytek Burgess CE, Vernet CAM, Li L, Gorman Guo X, Shenoy SG, Padigaru M, Taupier CAM, Gangoli EA, Gusev V, Snith Pochart PF, Fernandes ER, Shimkets RA, Larochelle WJ, Zhong M, Khramtsov NV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 223; 413pp; English.
                                                                                2001US-0275578P.
2001US-0275579P.
2001US-0275601P.
2001US-0276000P.
2001US-0276776P.
2001US-027694P.
2001US-0277339P.
                                                                                                                                                                                               2001US-02802329.
2001US-02808029.
2001US-02880529.
2001US-02880669.
2001US-0288289.
2001US-0298289.
                                    08-MAR-2002; 2002WO-US007355
                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-058423/05.
N-PSDB; ABX70491.
                                                                                                                                                                                                                      02-MAY-2001;
02-MAY-2001;
17-MAY-2001;
                                                                                                                                                                                                 0-MAR-2001;
                      10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer.
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SEQ ID NO: 96.

human NOVX polypeptide

Novel

1330

61

1505

22;

Gaps

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proteins, and the polynucleotide sequences encoding them. The NOVX proteins of the invention are G-protein coupled receptor (GPCR) related proteins. The sequences of the invention are useful in the manufacture of a medicament for treating a syndrome related to a human disease associated with the polypeptides e.g. cancer. ABUS2311-ABUS240B represent the human NOVX proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD---Y 118
                                                                                                                                                                                                                                                                                                                                                                                                                             231 SGLRCEEGVTVTTPSLSGAGSYLALPALTNTHHELR-------LDVEFKPLAP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 DGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 KDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSV 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 NGKRL------DLTYSFLGSQGIGQCYDSSPCER---OPCOHGATCMPAGEYERQC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              616 GRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITGCVKNL 673
                                                                                                                                                                                                              2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR
                                                                                                                                                                                                                                                                                                           119 GAIPKAGLSSGFIGCVRELRIQGEEIVFHDLNL-----TAHGISHC--PTCRDRPCQNG
                                                                                                                                                                                                                                                                                                                                                                      171 GOCHDSESSYVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYICRCHLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .506 EGTFCQ----TASGODGSGPFLA-DFNGFSHLELRGLHTFARDLGERMALEVVFLARGP
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                                                                                                                                                                 Indels 151;
                                                                                                                                     Length 1931;
                                                                                                                                  23.6%; Score 901.5; DB 6; 32.2%; Pred. No. 2.5e-48; ive 93; Mismatches 266;
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                                                                                                                                                Local Similarity 32.2%
les 242; Conservative
                                                                                                      Sequence 1931 AA;
                                                                                                                                  Query Match
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                                                                                                                                                  Best Loca
Matches
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The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
                                                    nootropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory, hypotensive; antiarteriosclerotic; hymostatic; osteopathic; gene therapy.; NOVX; diabetee; obesity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia; cardiomypathy; AIDS; asthma; Crohn's disease; multiple sclerosis; hypertension; atherosclerosis; hemophilia; graft-versus-host disease; Albright hereditary osteodystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spytek KA;
Zerhusen BD;
                                        antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and polynuclectides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kekuda R, Malyankar UM, Li L, Pena CEA, Spytek KA, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR, Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Zi, Ellerman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 96; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200105-0294134P-
200105-0294334P-
200105-0294837P-
200105-0306899P-
200105-0308991P-
200105-0312270P-
200105-03184346P-
200105-0318438P-
200105-0338683P-
200105-03388993P-
200105-03388993P-
200105-03388993P-
200105-03388999P-
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2001US-0289817P.
2001US-0289817P.
2001US-0290194P.
2001US-0290753P.
2001US-0291181P.
2001US-0291041P.
2001US-0292001P.
2001US-029201P.
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2001US-0293747P.
2001US-0294109P.
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N-PSDB; ADC39153.
                                                                                                                                                                                                     WO2003010327-A2
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Padigaru M, R
Edinger SR, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2001, 2
30-MAY-2001, 2
31-MAY-2001, 2
12-JUL-2001, 2
31-JUL-2001, 2
                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-2001;
21-MAY-2001;
22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2001;
25-MAY-2001;
29-MAY-2001;
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16-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2001;
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615

(first entry)

18-DEC-2003

ADC39154;

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----HPLHLLEDAVTKPELRPCPT 2052

2024 CLRDVVVGR---

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particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NoVX polypeptide. The NOVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide are especially useful for treating or preventing e.g. diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate cancers), dysliptidemiss, anorexia, wasting disorders, Altheimer's disease, parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's disease, multiple sclerosis, hypertension, atherosolerosis, hemophilia, graft-versus-host disease or Albright hereditary osteodystrophy. The DNA encoding the protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX proteins of the

Sequence 2053 AA;

24; 1623 1624 EGIFCQ----TASGQDGSGPFLA-DFNGFSHLELRGLHTIARDLGEKMALEAVFLARGP 1677 1907 .964 VAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALMLGGLPELPVGPALPKAYGTGFVG 2023 62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD---Y 118 119 GAIPKAGLSSGFIGCVRELRIQGEEIVFHDLNL-----TAHGISHC--PTCRDRPCQNG 170 230 231 SGLRCEEGVTVTTPSLSGAGSYLALPALTNTHHELR-------LDVEFKPLAP 276 GEVSVNGKRL------DLTYSFLGSQGIGQCYDSSPCER---QPCQHGATCMPAGE 438 550 610 668 277 DGVILFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERIN 336 337 KDGSLRVNGGRPVLRSSPGKSQG----LINLHTLLYLGGVEPSVPLSPATNMSAHFRGCV 391 439 YEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIA 498 61 IKITFRPDSADGMLLYNGOKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR GOCHDSESSSYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGR 1566 APCONLEAGRFHCOCPPGRVGPTCADEKS-PCOPNPCHGAAPCRVLPEG-GAOCECPLGR ||:|| |1908 EATQGLVI.MS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRMLRV 499 ESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET-----IELEVRT STASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRV 611 TALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPD--VATLTGGRFSSGITG 23.3%; Score 891.5; DB 7; Length 2053; 32.1%; Pred. No. 1.2e-47; ive 94; Mismatches 263; Indels 157; Gaps CVKNLVLHSARPGAPPOPLDLOHRAQAGANTRPCPS 705 Query Match 23.3% Best Local Similarity 32.1% Matches 243; Conservative N 392 1865 551 699 ò 셤 à 셤 8 d ò 셤 ठे d ઠે 셤 ઠે D ∂ g 8 g ò 셤 ò ે ઠે 셤

WPI; 2003-239445/23 N-PSDB; ADC39163.

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                                                                                                                   nootropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiatchmatic; antiinflammatory, hypotensive; antiateriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX; diabetes; obesity; cancer; lymptoma; uterus cancer; prostate cancer; dyslipidemia; ancrexia; wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia; cardiomypathy; AIDS; asthma; Crohn's disease; multiple sclerosis; hypertension; atherosclerosis; hemophilia; graft-versus-host disease; Albright hereditary osteodystrophy.
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, Zerhusen BD;
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Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen
M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR;
, Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, E
                                                                                                         antidiabetic; cytostatic; immunomodulator; anorectic;
                                                                                Novel human NOVX polypeptide SEQ ID NO: 106.
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            ADC39164 standard; protein; 2143
                                                                                                                                                                                                                                                                                                                                                                        2001US-0289818P.
2001US-0290194P.
2001US-0290753P.
2001US-0291181P.
2001US-029143P.
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2001US-0292587P.
2001US-0293107P.
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2001US-0304879P.
2001US-0308901P.
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2001US-0313416P.
2001US-0318463P.
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2001US-0294109P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0294110P.
2001US-0294434P.
                                                                                                                                                                                                                                                                                                    02-MAY-2002; 2002WO-US014199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-00136826
                                                         18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patturajan M, Anderson
Padigaru M, Rastelli L,
Edinger SR, Ellerman K,
                                                                                                                                                                                                                                                      WO2003010327-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001)
16-MAY-2001)
21-MAY-2001)
22-MAY-2001)
23-MAY-2001)
25-MAY-2001)
25-MAY-2001)
29-MAY-2001)
29-MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2001;
12-JUL-2001;
31-JUL-2001;
14-JUL-2001;
17-AUG-2001;
10-SEP-2001;
27-SEP-2001;
28-CT-2001;
28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2001;
11-MAY-2001;
14-MAY-2001;
                                                                                                                                                                                                                                                                                                                                       03-MAY-2001;
07-MAY-2001;
09-MAY-2001;
                                                                                                                                                                                                                               Homo sapiens.
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Gorman L,
                                   ADC39164;
ADC39164
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us-10-006-011a-3.rag

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The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid cor nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide are especially useful for treating or preventing e.g. diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate cancer), dyslipidemias, anorexia, wasting disorders, asthma. Crohn's disease, multiple solerosis, hypertension, atherosolerosis, hemophilia, cascoding the protein is useful in gane therapty for treating the above conditions. These are also useful in gane therapty for treating the above conditional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX proteins of the
  New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
                                                                                                                                    Claim 1; SEQ ID NO 106; 748pp; English.
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Sequence 2143 AA;

: : || |:||||| |: 1400 LALEFRALEPQGLLIYNGNA-----RGKDFLALALLDGRVQLRFDTGSGPAVLT 1448 1677 62 HPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD---Y 118 GAIPKAGLSSGFIGCVRELRIQGEEIVFHDLAL-----TAHGISHC--PTCRDRPCQNG 170 439 YEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIA 498 2 IKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATIR 61 171 GOCHDSESSYVCVCPAGFIGSRCEHSQALHCHPEACGPDAICVNRPDGRGYTCRCHLGR 1566 APCONLEAGREHCQCPPGRVGPTCADEKS-PCOPNPCHGAAPCRVLPEG-GAQCECPLGR 277 DGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLN GEVSVNGKRL-----DLTYSFLGSQGIGQCYDSSPCER---QPCQHGATCMPAGE QLVSLGGRQLLTPEHVLRQVDVT-SFAG------HPCTRASGHPCLNGASCVP---SGLRCEEGVTVTTPSLSGAGSYLALPALTNTHHELR------LDVEFKPLAP KDGSLRVNGGRPVLRSSPGKSQG-----LNLHTLLYLGGVEPSVPLSPATNMSAHFRGCV 247; DB 7; Length 2143; Indela 22.2%; Score 849.5; DB 7; 29.0%; Pred. No. 5.7e-45; tive 95; Mismatches 259; 246; Conservative Query Match Best Local Similarity Matches 246; Conserv 119 231 337 392 쉱 ઠે 엄 ଚ 셤 ઠે D, ઠે 셤 g ò ઠે 셤 à 유 ठे g

-----VEKSAG------DVDTLAFDGRTFVBYLNAVTESEKALQSNHFELSLRT 1907

1865

8

499 ESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPET-----IBLEVRT

1908 BATQGLVLWS----GKATERADYVALAIVDGHLQLSYNLGSQPVVLRSTVPVNTNRWLRV 1963 Ding L; Xu Y, Tran UK; Gandhi AR; Cell adhesion and extracellular matrix protein 8; CADECM-8; human; anti-HIV; virucide; antiallergic; antiniflammatory; antianaemic; antiallergic; anticonvilasan; antiinfertility; antiatreriosclerotic; anticonvilasan; antiinfertility; antiatreriosclerotic; antiethmatic; immunosuppressive, antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; antihyropic; antiparasitic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antiparasitic; antiparasitic; antiparasitic; antiparatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacatic; antipacterial; protozoacide; fungicide; gynaecological; gene therapy. 2084 GDSHCLCCRGLPRELPVGPALPKAYGTGFVGCLRDVVVGR------HPLHLLEDAVTKP 551 STASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRV 1964 VAHREQREGSLQVGNEAPVTGSSPLGATQLDTDGALWLGECFGETREGCPRVSDIRGTDS New human cell adhesion and extracellular matrix proteins, useful for diagnosing, treating or preventing autoimmune or inflammatory disorder (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis 611 TALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIG-----GAPDVATLTG---2024 TPORPPLSQGACEPAGWALFSRCSPCSSQCCGAGRRVPRCGPPAGHLLVGVPISITESQP ----FSSGITGCVKNLVLHSARPGAPPQPLDLQHRAQAGA Ramkumar J; Thangavelu K, Honchell CD, lick DA, Lee S, Warren BA, a AJA, Yao MG, Nguyen DB, G a JA, Chinn AM, Elliott VS, Human cell adhesion and extracellular matrix protein 8. Lee EA, Duggan BM, Thangavelu K, H JL, Baughn MR, Kallick DA, Lee S, Thornton M, Hafalia AJA, Yao MG, Walhia NK, Griffin JA, Chinn AM, S, Forsythe IJ; Claim 1; Page 157-159; 178pp; English. Ź ABP58231 standard; protein; 671 02-MAY-2001; 2001US-0288290P. 21-MAY-2001; 2001US-0292468P 28-JJN-2001; 2001US-0301672P. 01-MAY-2002; 2002WO-US013874 (INCY-) INCYTE GENOMICS INC. (first entry) 2136 ELRPCPT 2142 NTRPCPS 705 Khan FA, Walhia NK, Arvizu CS, Forsythe WPI; 2003-167112/16. N-PSDB; ABZ24585. Lee EA, WO200288322-A2 Homo sapiens. 31-MAR-2003 Yue H, Lee Hillman JL, Lal PG, Tho. 07-NOV-2002 669 662 ABP58231; 셤 셤 ઠે 셤 ઠે 셤 ઠે ଚ 셤

The present sequence is the protein sequence of Incyte polypeptide

2736276CD1 denoted human cell adhesion and extracellular matrix protein 8

(CADECM-8). The protein is encoded by a clone isolated from a soft tissue tumour cDNA library. The invention provides CADECM-1 to -11 polypeptides

(See ABP58224-34) and polynucleotides (see AB224578-88), vectors, host cells, antibodies, agonists and antagonists. These are useful for diagnosing, treating or preventing disorders associated with aberrant expression of CADECM, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal heemoglobiuuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental disorders (e.g. renal nocturnal namemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), reproductive disorders (e.g. infertility or a disruption in the menstrual cycle), or autoliditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomenlonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, heumatoid arthritis, syndrome, undections theumatoid arthritis, syndrome, undections theumatoid arthritis, fungal, or viral, bacterial, fungal, parasitic, protezoal or helminthic infections \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 671 AA;

셤 ò g à g ò a ò 엄 ò ద 8 g à g  $\dot{\delta}$ 셤 ò С ठे

230 DKQKIVEGMAEGGFTQIKCNTDIFIGGVPNYDDVKKNSGVLKPFSGSIQKIILNDRTIHV 433 522 DDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDG 581 641 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD-YG 119 120 AIPKAGLSSGFIGCVRELRIQGEEIVFHDLN-----LTAHGISHCPT--CRDRPCQNG 170 183 LVRATGTNRGFQGCVQSLAVNGRRI----DMRPWPLGKALSGADVGECSSGICDEASCIHG 239 SGLRCEEGVTVTTPSL-SGAGSYLALPALTNTFHEL---RLDVEFKPLAPDGVLLFS--- 283 KGRHCEDAFTLTIPQFRESLRSYAATPWPLEPQHYLSFMEFEITFRPDSGDGVLLYSYDT 318 GGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEPLALGRWHRVSAERLNKDGSLRV 343 344 NGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPATNMSAHFRGCVGEVSVNGKRLDL 403 404 TYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQL 463 434 KHDF--TSGVNVENAAHPCVRAPCAHGGSCRPRKE-GYDCDCPLGFEG------ 478 505 POILKRVSG---SRS----NVFMRFKTTAKOĞLLIMRG--DSPMRPNSDFISLGIRDG 553 642 AKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTR 701 123 VSETKIKLGGWHTVMLYRDGLNGLLQLNNGTPVTGQSQGQYSKITFRTPLYLGGAPSAYW 182 REPCLHGGTCQGT--RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFH 521 582 HLVFRYOLGSGEARLVSEDPINDGEWHRVTALREGRRGSIOVDGEELVSGRSFGPNVAVN GOCHDSESSSYCCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGR Query Match 22.0%; Score 840; DB 6; Length 671; Best Local Similarity 29.6%; Pred. No. 6e-45; Matches 214; Conservative 107; Mismatches 257; Indels 144; Gaps 1 EIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI GTCTAIKADŚYICLCPLĠF------72 61 240 231 259 284 319 374 464 Query Match

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The invention relates to a novel isolated human neurotransmission-associated proteins (NTRAM) polypeptide. The polypeptide of the invention demonstrates cytostatic and immunomdulator activities and may be useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of gene therapy procedures. The current sequence is that of the human NTRAM protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human neurotransmission-associated proteins (NTRAN) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of NTRAN e.g., cancer.
61 RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD-YG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIKITFRFDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 QITLEFRAEABDGLLLYCGENE-----HGRGDFWSLAIIRRSLQFRFNCGTGVAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214; Conservative 107; Mismatches 257; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baughn MR, Bhatia U, Blake JJ, Burrill JD, Elliott VS; Emerling BM, Forsythe IJ, Gietzen KJ, Gorvad AE, Griffin JA; Hafalia AJA, Ho A, Jackson AA, Jiang X, Kable AE, Kearney L, Khare R, Lee EA, Lee S, Lu DAM, Marquis JP, Lehr-Mason PM; Ramkumar J, Richardson TW, Sprague WW, Tran UK, Chawla NK; Warren BA, Yue H, Zheng W;
                                                                                                                                                                                                                                                                                                      human; neurotransmission-associated protein; NTRAN; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1009;
                                                                                                                                                                                                                                                                                                                      immunomodulator; immune disorder; cancer; gene therapy.
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29.6%; Pred. No. 9.6e-45;
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                                                                                                                                                                      ADE28105 standard; protein; 1009 AA.
                                                                                                                                                                                                                                                                     Human NTRAN protein - SEQ ID 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 2002US-0365645P.
, 2002US-0367662P.
, 2002US-0379887P.
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18-MAR-2002; 2002US-0365645P.
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461 VSETRIKLGGWHIVMLYRDGLNGLAGLANGTPVTGQSQGQYSKITFRTPLYLGGAPSAYW 520
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developmental defect; inflammatory disease; dermatological; vulnerary;
immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 REPCLHGGTCQGT--RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFH
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The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation healing and in modulating immune responses. The present sequence is a polypeptide of the invention

Sequence 819 AA;

Query Match

Best Loca Matches

New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for

Claim 4; Page 308-310; 466pp; English.

growth and developmental desmodulating immune responses

Murison JG;

Onrust R,

Sleeman M,

'n

Strachan

Watson JD, Kumble KD;

WPI; 2002-122020/16

(GENE-) GENESIS RES & DEV CORP LTD.

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RHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDLNEELYLGGYPD-YG 119
                                                                                                                                                         120 AIPKAGLSSGFIGCVRELRIQGEEIVFHDLN-----LTAHGISHCPT--CRDRPCQNG 170
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                                                                    1 BIKITFRPDSADGMLLYNGQKRVPGSPTNLANRQPDFISFGLVGGRPEFRFDAGSGMATI
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388 GTCAAIKADSYICLCPLGFRGR.----
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WO200190357-A1

Rattus sp

29-NOV-2001

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABL16176-ABL36511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                    YIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPC 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                       developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 17634
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                                                                                                   ABB63614 standard; protein; 4072 AA
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11-JUL-2000; 2000US-00614150.
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N-PSDB; ABL07717.
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180 SYVCVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEBGV 239

123 KAGLSS--GFIGCVRELRIQGEEIVFHDLNLTAHGISHCPTCRDRPCQNGGQCHDSES-S 179

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                                                                                                                        240 TVTTPSLSGAGSYLA---LPALTNTHHELRLDVEFKPLA-PDGVLLFSGGKSGPVEDFVS
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N-PSDB; ABL06051.
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10-MAY-1996;
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                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, therapeuticy and pharaceutical furge. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence date for this patent dd not form part of the printed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                 17.4%; Score 664.5; DB 4; Length 1298; larity 22.0%; Pred. No. 1.7e-33; Conservative 111; Mismatches 295; Indels 379;
                                     Disclosure; SEQ ID NO 12636; 21pp + Sequence Listing; English
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Matches 221; Conserv
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                                              1077 LEQHTSSTPQTHTDWSLLKKFDLSAEHQSQVQGVRKNFGACFAGSDSYFHYNDADTMSQV
                                                                                                533 FSRSLPEVPETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSG
                                                                                                                                                                                                      EARL-VSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGA
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ligand; muscle atrophy; muscular dystrophy; myopathy; diagnosis;
gene therapy.
                                                                                                                                                                                                                                                                                                                                             PDVATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAG 697
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|abel= Sig_peptide
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--- "Claim 2"
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"sequence
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324. .331
/label= Z-
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ADC39166;

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278
                                                                                                                                                                       This polypeptide comparises the amino acid sequence of human agrin deduced from an isolated foetal brain cDNA clone (see AR79041). Pull-length agrin, or active portions of it, can be expressed using a claimed host-vector system. The agrin polypeptides can be used in claimed methods treating diseases or disorders that affect muscle, especially atrophy resulting from denervation due to nerve trauma, degenerative, metabolic or inflammatory neuropathy, peripheral neuropathy or damage to nerves caused by environmental toxins or drugs. In particular the muscle atrophy is due to motor neuronopathy, chronic disuse, metabolic stress or nutritional insufficiency, muscular dystrophy syndrome, congenital myopathy or acquired (toxic or inflammatory) myopathy. The polypeptides can also be used in a claimed method of promoting the growth, if elecantiation or survival of cells that express muscle-specific (MuSK) receptors (see AAM26610-11), and to raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 IGQCYDSSPCER---QPCQHGATCMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLH 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VCLCPGGFSGPHCEKGL-----VEKSAG-----DVDTLAFD 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
Nucleotide sequences encoding human agrin and muscle specific kinase and related receptor - used in diagnosis and treatment of disorder with muscle atrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 CHPEACGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPALTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQPNPCHGAAPCRVLPEG-GAQCECPLGREGTFCQ----TASGQDGSGPFLA-DFNGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HHELR--------LDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.7%; Score 640.5; DB 2; Length 492;
Best Local Similarity 33.0%; Pred. No. 1.9e-32;
Matches 183; Conservative 59; Mismatches 173; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 15; 120pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 492 AA;
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ADC39166 standard; protein; 1566 AA.

RESULT 14 ADC39166 ID ADC39

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                                                                             antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic; nootropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive; antiatersinsolerotic; hemostatic; osteopathic; gene therapy.; NOVX; diabetes; obssity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia; antiopathy; AlS; asthma; Crohn's disease; multiple sclerosis; hypotension; atherosclerosis; hemophilia; graft-versus-host disease; Albright hereditary osteodystrophy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spytek KA;
, Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and polymucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ďŖ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miller CE, Kekuda R, Malyankar UM, Li L, Pena CEA, Spytek F Gorman L, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhus Patuturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall J Padigaru M, Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Edinger SR, Ellerman K;
                                                           SEQ ID NO: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 108; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    200105-0290139F
200105-0290739F
200105-02912819F
200105-0292011F
200105-0292011F
200105-0292074F
200105-0293107F
200105-0293107F
200105-0293107F
200105-0294109F
200105-0294109F
200105-0294109F
200105-0294109F
200105-0294109F
200105-0294109F
200105-0294100F
200105-0294109F
                                                           Novel human NOVX polypeptide
                                     18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-239445/23.
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                                                                                                                                                                                                                                             WO2003010327-A2
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10-SEP-2001; 27-SEP-2001; 2
18-OCT-2001; 28-NOV-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2001;
18-MAY-2001;
22-MAY-2001;
23-MAY-2001;
23-MAY-2001;
29-MAY-2001;
29-MAY-2001;
30-MAY-2001;
31-MAY-2001;
31-MAY-2001;
31-MAY-2001;
31-MAY-2001;
12-MAY-2001;
14-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-2001;
14-MAY-2001;
15-MAY-2001;
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           09-MAY-2001;
                                                                                                                                                                                                                                                                       06-FEB-2003
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Human, pharmaceutical, diagnostic, gene therapy, tissue regeneration, cell regeneration, membrane protein, signal transduction-related protein, transcription-related protein, osteoporosis, neurological disease,

cancer; tumour Homo sapiens. EP1308459-A2 37-MAY-2003.

The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NoVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and inabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, parkinson's disorder, cachesta, cardiomyopathy, AIDS, asthma, Crohn's parkinson's disorder, cachesta, cardiomyopathy, AIDS, asthma, Crohn's graft-versus-host disease or Albright hereditary osteodystrophy. The DNA encoding the protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX proteins of the invention. 

Sequence 1566 AA;

Ishii S; ;, Tamechika I;

(HELI-) HELIX RES INST. (REAS-) RES ASSOC BIOTECHNOLOGY.

famamoto J, H

Bogai

28-MAR-2002; 2002EP-00007401. 05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.

> 1170 1230 1517 16; 1291 DFSKLARAAAVSSGFDGAIQLVSLGGRQLLTPEHVLRQVDVT-SFAG------HPC 1339 1363 1402 VTESEKALQSNHFELSLRTEATQGLVLWS----GKATERADYVALAIVDGHLQLSYNLGS 1457 312 372 479 1364 CPGGFSGPHCEKGL------VEKSAG------DVDTLAFDGRTFVEYLNA 1401 266 422 480 CLPGFSGPRCOOGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPE 539 591 592 GEARLVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGA 651 207 CGPDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSLSGAGSYLALPALTNTHHELR ------LDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGHLEFRYELGSG LAVLRSABPLALGRWHRVSABRLNXDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVE PSVPLSPATNMSAHFRGCVGEVSVNGKRL-----DLTYSFLGSQGIGQCYDSSPC 423 ER---QPCQHGATCMPAGEYEPQCLCRDGFKGDLCEHEBNPCQLREPCLHGGTCQGTRCL VPET-----IELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGS 1458 QPVVĽRSTVPVNTNRWIRVVAHREQREGSLÓVGNBAPVTGSSPLGATQLDTDGALWLGGL Gaps PD--VATLTGGRFSSGITGCVKNLVLHSARPGAPPPQPLDLQHRAQAGANTRPCPS 705 16.6%; Score 635.5; DB 7; Length 1566; 33.4%; Pred. No. 1.5e-31; ive 58; Mismatches 174; Indels 125; Query Match
> Best Local Similarity 33.4%
> Matches 179, Conservative 313 540 1518 373 652 267 ద 셤 a 셤 ઠ 쉱 ઠે g ò g ଟ ઠે ઠે  $\delta$ ò ઠે

The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nuclectide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polymuclectide or its patrial peptide, an antibody binding to the polypeptide or peptide of the polymuclectide, immunologically assaying the polypeptide or peptide with the antibody of the encoded by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymuclectide in an expressible manner and an antisense polymuclectide. The oligonuclectide is useful as a primer for synthesishing the polymuclectide, or as a probe for detecting the polymuclectide. The polymuclectide and encoded genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of genes may be more are involved in tissue and/or cell captacine, are involved in tissue and/or cell captacine, and penes are involved in tissue and/or cell captacine, as a probe an expression. Membrane proteins, disease-related proteins, transcription related proteins, disease-related proteins and genes and manner plans and activity, or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an encoder and activity or an neurological diseases, cancer, tumours. The cDNA may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or encoding them can be used as indicators for diseases (e.g. osfeoporosis, neurological diseases, cancer, tumours. The CDNA may be used to regulate Otsuki T, Wakamatsu A, Sato H, Isl Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y; Claim 1; Page; 222pp; English. as targets of gene therapy Query Match Best Local Similarity 28.74 Matches 162; Conservative Sugiyama T, J, Isono Y, Y 2003-450961/43 N-PSDB; ADB62934. Sequence 463 AA; 21 Seki N, d ઠે ઠે ద Ź ADB64904 standard; protein; 463 04-DEC-2003

LTAHGISHCPT--CRDRPCQNGGQCHDSESSYVCVCPAGFTGSRCEHSQALHCHPEACG 208 -RLDVEFKPLAPDGVLLFS---GGKSGPVEDFVSLAMVGGHLEFRYELGSGLAVLRSAEP 321 ------KGRHCEDAFTLTIPOFRESLRSYAATPWPLEPQHYLSF 209 PDATCVNRPDGRGYTCRCHLGRSGLRCEEGVTVTTPSL-SGAGSYLALPALTNTHHEL--16.4%; Score 628; DB 7; Length 463; 28.7%; Pred. No. 1.1e-31; ive 80; Mismatches 198; Indels 124; 

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Human protein encoded by clone PLACE60113340.

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DT 04-1
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89 MEFEITFRPDSGDGVLYSXDTGSKDFLSINLAGGHVEFRFDCGSGTGVLRSEDP 143	322 LALGRWHRVSAERLUKDGSLRVNGGRPVLRSSPGKSQGLNLHTLLYLGGVEPSVPLSPAT 381	144 LTLGNWHELRVSRTAKNGILQVDKQKIVEGMAEGGFTQIKCNTDIFIGGVPNYDDVKKNS 203	· • -	204 GVLKPFSGSIQKIIINDRTIHVKHDFTSGVNVENAAHPCVRAPCAHGGSCRPRKE-GY 260	442 QCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGIAE 499	261 DCDCPLGFEG	500 SDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLW 559	289RSYLIYDNPDILKRVSGSRSNVFMRFKTTAKDGLLLW 325	560 QGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRG 619	326 RGDSPMRFNSDFISLGLRDGALVFSYNLGSGVASIMVNGSFNDGRWHRVKAVRDGQSG 383	GAPDVATLTGGRFSSC	384 KITVDDYGARTGKSPGMMRQLNINGALYVGGMKEIALHTNRQYMRGLVGCISHFTLST 441	680 PGAPPPQPLDLQHRAQAGANTRPC 703	442DYHISLVEDAVDGKNINTC 460	
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Search completed: March 9, 2004, 17:19:02 Job time: 91.8465 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 9, 2004, 17:11:52; Search time 6.86906 Seconds (without alignments) 2152.832 Million cell updates/sec

US-10-006-011A-9 1566 1 CERQPCQHGATCMPAGEYEF.....QPLDLQHRAQAGANTRPCFS 284 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMABIES

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SUMMARIES	QI .	PGBM HUMAN	PGBM_MOUSE	UN52 CAEEL	AGRI_RAT		AGRI_CHICK	FAT DROME	SLTZ HUMAN	FAT2 DROME	STAN DROME	LMA2 HUMAN	NX3A RAT	CLR2_HUMAN	CLR2 RAT		CLR3_HUMAN		CLR3_RAT	NX3A_HUMAN	NTC3_HUMAN	CLR1_HUMAN	NX1A_BOVIN	NX2A_RAT	NXIA_CHICK	NX1A HUMAN	NX1A_RAT	CLR1 MOUSE			LMA1_HUMAN		LML2_CAEEL	CADN_DROME
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## ALIGNMENTS

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[1] — SEQUENCE FROM N.A. MEDLINE=92112994; PubMed=1730768; Kallunki P., Trygyvason K.; Kallunki P., Trygyvason K.; Kallunki P., Trygyvason K.; Kallunki P., Trygyvason K.; Kallunki P., Trygyvason K.; Kallunki Dasement membrane heparan sulfate proteoglycan core protein a 467-kD protein containing multiple domains resembling elements of the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor."; Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
MEDLINE=20553141; PubMed=11101850;
Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
Hentati F., Fontaine B.;
"Perlecan, the major proteoglycan of basement membranes, is altered in
patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
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FIRSUBECCION, and Skin;

MEDLINE-92235084; PubMed=1569102;

MIDLINE-92235084; PubMed=1569102;

Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;

Primary structure of the human heparan sulfate proteoglycan from
"Primary structure of the human heparan sulfate proteoglycan from
"Primary structure of the human heparan sulfate proteoglycan from
"Primary structure of the low density lipoprotein receptor, laminin,
neural cell adhesion molecules, and epidermal growth factor.";
". Biol. Chem. 267:8544-8557(1992).
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"Heperan sulfate proteoglycan of human colon: partial molecular cloning, cellular expression, and mapping of the gene (HSPG2) to the short arm of human chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                           P98160; Q16287; Q9H3V5; Orcated) Cror1-196 (Rel. 34, Created) 10-0CT-1996 (Rel. 34, Last sequence update) 10-0CT-2003 (Rel. 42, Last sequence update) Basement membrane-specific heparan sulfate proteoglycan core procein precursor (HSPG) (Perlecan) (PLC).
                                                                                  4391 AA
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MEDLINE=91365376; PubMed=1679749;
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SEQUENCE OF 890-1396 FROM N.A.
TISSUE=Flbrosarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        C --- SUBCELLULAR LOCATION: Extracellular.

C --- TISSUE SPECTFICITY: Found in the basement membranes.

--- TISSUE SPECTFICITY: Found in the basement membranes.

--- TISSUE SPECTFICITY: Found in the basement membranes.

AND O-LINKED OLIGOSACCHARIDES.

--- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel.

C STAGASE: Defects in HSPG2 are the cause of Schwartz-Jampel.

C Anaracterized by permanent myotonia (prolonged failure of muscle relaxation) and skeletal dysplasia, resulting in reduced stature, kyphosocoliosis, bowing of the diaphyses and irregular epiphyses.

C --- SIMILARITY: Contains 1 laminin BGF-like domains.

--- SIMILARITY: Contains 2 laminin IV domains.

C --- SIMILARITY: Contains 3 laminin G-like domains.

C --- SIMILARITY: Contains 3 laminin G-like domains.

C --- SIMILARITY: Contains 4 EGR-like domains.

C --- SIMILARITY: Contains 4 EGR-like domains.
                                                                                                                                                                                                                          CARBOHYDRATE-LINKAGE SITE ASN-2121.

MEDLINE-22660472; PubMed=12754519;

Albang H., Li X.-J., Martin D.B., Aebersold R.;

Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";

Nat. Blotechnol. 21:660-666(2003).

-! FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells.

-!-SUBDNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type
                                                                                                           [6] SEQUENCE OF 1-21 FROM N.A. SEQUENCE OF 1-21 FROM N.A. MEDLINE=94052171; PubMed=8234307; Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.; Structural characterization of the complete human perlecan gene and
MEDLINE=92120660; PubMed=1685141; Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B., Tryggvason K.; "Cloning of human heparan sulfate proteoglycan core protein, assignment of the gene (HSPG2) to 1p36.1-->p35 and identification of Genomics 11:389-396(1991).
                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008985; Cona like_lec_gl.
InterPro; IPR00742; EGF_Z.
InterPro; IPR006210; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-like.
InterPro; IPR003599; Ig-c.
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EMBL; M85289; AAA5700.1; --
EMBL; AL445795; CAC18534.1; --
EMBL; AL445795; CAC18534.1; --
EMBL; N64283; AAA52699.1; --
EMBL; S76436; AA85121.2; --
EMBL; L22078; --
FIR; A38096; A38096.
FIR; A38096; A38096.
FIR; P00740; 1EDM.
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FIR; P0075573; HSPG2.
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MIM; 255800; -.
                                                                                                                                                                                    its promoter.";
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R SMART; SW00409; IG; 22.

R SMART; SW00409; IG; 22.

R SMART; SW00409; IG; 22.

R SMART; SW00281; LamB; 3.

R SMART; SW00282; LamB; 3.

R SMART; SW00229; LamB; 3.

R SMART; SW00220; EdF 1; 9.

R PROSITE; PS00022; EGF 2; 6.

R PROSITE; PS00025; EGF 2; 6.

R PROSITE; PS00025; LAM G DOMAIN; 3.

R PROSITE; PS0029; LDLRA 1; 4.

R PROSITE; PS00209; LDLRA 1; 4.

R PROSITE; PS0043; LAMINT TYPE EGF; 11.

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R PROSITE; PS0043; LDLRA 1; EGF-1ike domain; Immunoglobulin domain; M Extracellular matrix; EGF-like domain; Immunoglobulin domain; M Extracellular matrix; EGF-like domain; Disease mutation.

T SIGMAL 1.
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IGALINE C2-TYPE 1.
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BASEMENT MEMBRANE-SPECIFIC HEPARAN
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LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
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C2-TYPE 6.
C2-TYPE 7.
C2-TYPE 9.
C2-TYPE 9.
InterPro; IPR003596; Ig_v.
InterPro; IPR000349; Laminin_B.
InterPro; IPR0002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001792; LDL receptor_A.
InterPro; IPR000189; SEA_domain.
Promos; SEA_i aminin_G.
Pram; Pr00053; laminin_G.
Pram; Pr00054; laminin_G.
Pram; Pr00054; laminin_G.
Pram; Pr00054; laminin_G.
Pram; Pr00054; laminin_G.
Prem; Pr00054; laminin_G.
Prem; Pr00054; laminin_G.
Propom; Pr00051; LinterErPror.
Propom; Pr00051; LinterErPror.
Propom; Pr00051; Laminin_B; 3.
SWART; SW00181; EGF. 15.
SWART; SW00181; EGF. 15.
SWART; SW00408; IGG2; 21.
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MEDLINE=22078153; PubMed=1744087;
Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M.,
Namada Y., Hassell J.R.;
"The complete sequence of perlecan, a basement membrane heparan
sulfate proteoglycan, reveals extensive similarity with laminin A
chain, low density lipoprotein-receptor, and the neural cell adhesion
molecule...;
J. Biol. Chem. 265:22939-22947(1991).
                                                                                                                                                                 61 PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVP
                                                                                                                                                                                                                                         ETIELEVRISTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
                                                                                                                                                                                                                                                               4228 ETIELEVRTSTASGLLIMQGVEVGEAQQCKDFISLGLQDGHLVFRYQLGSGEARLVSEDP
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                                                                                         1 CEROPCOHGATCMPAGEYEROCLCRDGFKGDLCEHEENPCOLREPCLHGGTCQGTRCLCL
                                                     Gaps
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-!- TISSUE SPECIFICITY: Found in the basement membranes.
-!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
-!- SIMILARITY: Contains 4 LDL-receptor class A domains.
-!- SIMILARITY: Contains 11 laminin EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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1D 10.NOV-1995 [Rel: 32, Last sequence update)

1D 10.NOV-1995 [Rel: 42, Last sequence update)

1D 10.CCT-2003 [Rel: 42, Last sequence update)

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Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 284; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                           SEA.
LIDL-RECEPTOR CLASS A 1.
LIDL-RECEPTOR CLASS A 2.
LIDL-RECEPTOR CLASS A 3.
LIDL-RECEPTOR CLASS A 4.
LIDL-RECEPTOR CLASS A 4.
LIGHIN BGF-LIKE 1 (N-TERMINAL).
LAMININ BGF-LIKE 1 (DOMAIN III A).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 2.
-1- SIMILARITY: Contains 3 laminin IV domains.
-1- SIMILARITY: Contains 15 immunoglobulin-like C2-type domains.
-1- SIMILARITY: Contains 3 laminin G-like domains.
-1- SIMILARITY: Contains 1 EGP-like domain.
-1- SIMILARITY: Contains 1 SEA domain.
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LAMININ EGF-LIKE 4 (INCOMPLETE).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 6.
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LAMININ EGF-LIKE 11.
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MEDLINE=93339574; PubMed=8393416;
Rogalski T.M., Williams B.D., Mullen G.P., Moerman D.G.;
Products of the unc-52 gene in Caenorhabditis elegans are homologous to the core protein of the mammalian basement membrane heparan sulfate proteoglycan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS, AND ALTERNATIVE SPLICING.

Durbin R.;

Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Probable role in myofilament assembly and/or attachment of the myofilament lattice to the cell membrane. May be an extracellular anchor for integrin receptors in muscle.

-!- SUBCELULAR LOCATION: Extracellular matrix.

-!- ALTERNATIVE PRODUCTS:

EVENT ENDING PRODUCTS:

Name a strike splicing; Named isoforms=4;
                                                                                                                                                                                                                                                   CERQPCRNGATCMPAGEYEFQCLCQDGFXGDLCEHEENPCQLHEPCLNGGTCRGARCLCL
                                                                                                                                                                                                                                                                                               PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPQQYGAYFHDDGFLAFPGHVFSRSLPEVP
                                                                                                                                                                                                                                                                                                               3604 INDGEWHRITALREGQRGSIQVDGEDLVTGRSPGPNVAVNTKDIIYIGGAPDVATLTRGK
                                                                                                                                                                                                                                CEROPCOHGATCMPAGEYEFOCLCRDGFKGDLCEHEENPCOLREPCLHGGTCOGTRCLCL
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006551; 018261; 018263; Q9XTD2; Q9XT15;
01-707-1994 [Rel. 29, Created)
10-077-2003 [Rel. 42, Last sequence update)
10-077-2003 (Rel. 42, Last sequence update)
Basement membrane proteoglycan precursor (Perlecan homolog)
(Uncoordinated protein 52).
Caenorhabditis elegans.
Caenorhabditis elegans.
Bukaryota; Metazoda; Nemacoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                               DB 1; Length 3707;
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STRAIN=Bristol N2;
Percy C.M. Baynes C.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               Pred. No. 1.4e-89
20; Mismatches 18
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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EMBL; 29395; CAB0780; IGA; 17.
EMBRT; SM00408; IGG.17.
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R PROSITE; P850028; LAM G DOMAIN; 3.

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| LOL-RECEPTOR CLASS A 2. |
| LOL-RECEPTOR CLASS A 3. |
| LOL-RECEPTOR CLASS A 3. |
| LOL-RECEPTOR CLASS A 3. |
| LOLIKE C2-TYPE 2. |
| LAMININ EGF-LIKE 1. (INCOMPLETE). |
| LAMININ EGF-LIKE 2. (N-TERMINAL). |
| LAMININ EGF-LIKE 2. (N-TERMINAL). |
| LAMININ EGF-LIKE 3. (INCOMPLETE). |
| LAMININ EGF-LIKE 4. (N-TERMINAL). |
| LAMININ EGF-LIKE 5. |
| LAMININ EGF-LIKE 6. |
| LAMININ EGF-LIKE 6. |
| LAMININ EGF-LIKE 7. |
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| LAMININ EGF-LIKE 6. |
| LALIKE C2-TYPE 3. |
| G-LIKE C2-TYPE 4. |
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SUBUNIT: Binds to laminin. Synaptic basal lamina at the neuromuscular SUBCELLULAR LOCATION: Synaptic basal lamina
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                                                                                                                                                                                                                                                                                                                                                                           IsoId=P25304-4; Sequence=VSP_001367;
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                                                                                                                                                                                                                    IsoId=P25304-1; Sequence=Displayed;
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KAZAL-LIKB 1
KAZAL-LIKE 2
KAZAL-LIKE 3
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LAMININ TYPE EGF; 1.
SEA; 1.
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InterPro; IPR008985; ConA like_lec_gl.
InterPro; IPR006209; EGF_like.
InterPro; IPR003345; FolM.
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Interpro; IPR00345; FolN.
Interpro; IPR00345; KalN.
Interpro; IPR00249; Laminin EGF.
Interpro; IPR001791; Laminin G.
Interpro; IPR001791; Laminin G.
Interpro; IPR000081; SEA_domain.
Pfam; PF00008; EGF, 4.
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EMBL; M64780; AAA40702.1; ALT_INIT.
EMBL; S44194; AAB23326.1; -.
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Pfam; Provided; Laminin_EGF; 2.
Pfam; PP00053; laminin_EGF; 2.
Pfam; PP01390; SRA; 1.
PRINTS; PR00119; BCFLam; 2.
SMART; SM00219; EGFLam; 2.
SMART; SM00220; KAZAL; 9.
SMART; SM00220; Lamid; 3.
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Laminin EGF-like domain,
SIGNAL
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tein; EGF-like
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HSSP; P00740; 1EDN
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           DNYREVDGRSTGILAMLNVDGNIFVGGVPDISKATGGLFSNNFVGCIADVELNGVK--- 3343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3178 ------PIEHAARFDGDAFIELSSDEFPHLTSEKDEIVAFKFKTEQQNGVLLMQG-Q 3227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3228 RPTVQQMEDYISVGIVNGHLHFSYELGGGAAHLISEERVDDGKEHSVRFERKGREGQMRI 3287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 LEGSGGNDAPGQYGAYFHDDGFLAFPGHVPSRSLPEVPETIELEVRISTASGLLLWQGVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 VGEAGQGKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLTGGRFSSGITGCVKNLVLHSARPGAP 262
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-! FUNCTION: Component of the basal lamina that causes the -! FUNCTION: Component of the basal lamina that causes the aggregation of acetylcholine receptors and acetylcholine-esterase on the surface of muscle fibers of the neuromuscular junction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 GDLCEHEE -- NPCOLREPCLHGGTCQGTR-----CLCLPGFSGPRCQQGSGHGIAESDWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3129 GDVYSTQEPNNIC-ANSTCGMNGQCVPRNMTHYTCECKLYYDGPTCSLFK-----
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 349; DB 1; Length 3375;
Pred. No. 6.5e-17;
.; Mismatches 102; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
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TISSUE=Embryonic spinal cord,
MEDILINE=9122570; PubMed=1851019;
Rupp F., Payan D.G., Magill-Solc C., Cowan D.M., Scheller R.H.;
"Structure and expression of a rat agrin.";
Neuron 6:811-823 (1991).
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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31.2%; Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81, Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insola-P25304-5; Sequence=VSP_001368;
-!- TISSUB SPECIFICITY: Embryonic nervous system and muscle.
-!- DEVELOPMENTAL SAGGE: More abundant early in development.
-!- DTM: Contains heparan sulfate chains as well as N-linked and O-linked oligosaccharides (By similarity).
-!- SIMILARITY: Contains 9 Kazal-like domains.
-!- SIMILARITY: Contains 2 laminin EGF-like domains.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 4 EGF-like domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
junction.
-!- ALTERNATIVE PRODUCTS:
    Event-Alternative splicing; Named isoforms=5;
    Comment=Additional isoforms seem to exist. Isoforms differ their acetylcholine receptor clustering activity;
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(POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
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/FTIG=VSP 001367.
Missing (In isoform 5).
/FTIG=VSP 001368.
V -> VTCD (IN A VARIANT).
MW; 7FEFDFDAFF89CC31 CRC64;
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KAZAL-LIKE 4.
KAZAL-LIKE 5.
KAZAL-LIKE 6.
KAZAL-LIKE 7.
KAZAL-LIKE 7.
LAMININ EGF-LIKE 1
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EGF-LIKE 4.
LAMININ G-LIKE 3.
SER/THR-RICH.
SER/THR-RICH.
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                                                                                                KAZAL-LIKE 9
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DB 1; Length 1959;

Score 333.5; DB 1 Pred. No. 4.5e-16;

21.3%; 36.0%;

Query Match Best Local Similarity

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1547
 10;
                                                       1444 CLPNPCHGGALCOALEAGMFLCOCPPGRFGFTCADEKSPCQ-PNPCHGAAPCRVLSSGGA 1502
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    56 RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSR 114
                                                                                                                                                 115 SLPEVPETIELEVRTSTASGLLLWQGVEVGEAGQGKDFISLGLQDGHLVFRYQLGSGEAR 174
                                                                                                         1 CEROPCOHGATCMPAGEYEROCLCRDGFKGDLCEHEENPCOLREPCLHGGTCQ----GT
                                                                                                                                                                                                           175 LVSEDPINDGEWHRVTALREGRRGSIQVDGEELVSGRSPG----PNVAVNAKGSVYIGGA
 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

--- SUBCELLULAR LOCATION: Synaptic basal lamina at the neuromuscular junction (By similarity).

--- SIMILARITY: Contains at least 2 laminin EGF-like domains.

--- SIMILARITY: Contains at least 3 EGF-like domains.

--- SIMILARITY: Contains 1 SEA domain.

--- SIMILARITY: Contains 3 laminin G-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Discopyge ommata (Electric ray).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoldea;
Torpediniformes; Narcinoidei; Narcinidae; Discopyge.
 28; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            PRT; 1328 AA
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PIR; T43060; T43060.
HSSP; P00740; 1EDM.
INTERPRO; IPR000153; ABX hydroxyl S.
INTERPRO; IPR008985; CONA like_lec_gl
InterPro; IPR008985; CONA like_lec_gl
                                                                                                                                                                                                                                                                                       1664 PDFSKLARGAAVSSGFSGVIQ 1684
                                                                                                                                                                                                                                                                   231 PDVATLT-GGRFSSGITGCVK 250
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94; Conservative
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InterPro; IPR006209; Ed
InterPro; IPR003645; F
InterPro; IPR002560; K
InterPro; IPR002049; Li
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  990 AVLRSKAPIPLNVMNVVTVERNGRKGLMKINKDELVSGESPKSRKAPHTALNLKEAFYVG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differ in function and distribution.";

Neuron 8:691-699(1992).

-[- FUNCTION: Component of the basal lamina that causes the aggregation of acetylcholine receptors and acetylcholine-esterase on the surface of muscle fibers of the neuromuscular junction.

-[- SUBGRILUMAR LOCATION: Synaptic basal lamina at the neuromuscular contacts.
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=3;
Comment=Additional isoforms seem to exist. Isoforms differ in
their acetylcholine receptor clustering activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Kroeger S., McMahan U.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92232299; Pubmed=1314621;
Ruegg M.A., Tsim K.W.K., Horton S.E., Kroeger S., Escher G.,
Gensch E.M., McMahan U.J.;
                                                                              1050 GAPDFNKFARAAG--IISGFTGAIQKLSLKS 1078
                                                                                                                                                                                                                                                     01-001-1993 (Rel. 26, Created)
01-001-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                   229 GAPD---VATLIGGRFSSGITGCVKNLVLHS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=P31696-1; Sequence=Displayed
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EMBL, M97371; AAA48586.1; -.
EMBL, M97372; -; NOT ANNOTATED_CDS.
PIR, JH0591; AGCH.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
MEDLINE=92232297; PubMed=1314620;
Tsim K.W.K., Ruegg M.A., Escher G
"cDNA that encodes active agrin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuron 8:677-689(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P31696;
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(POTENTIAL).
(POTENTIAL).
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NON TER 1
DOMĀIN 79 132 LAMININ EGF-1787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INKED (GLCNAC. . .) (POINT 19D81CLAF2A71Cl8 CRC64;
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LAMININ EGF-LIKE 2.
SEA.
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LAMININ G-LIKE 1.
EGF-LIKE 2.
LAMININ G-LIKE 2.
EGF-LIKE 3.
LAMININ G-LIKE 3.
                                                                                                                                                                                                                                                                           Pfam; PF00053; laminin EGF; 2. Pfam; PF00054; laminin G; 3. Pfam; PF01390; SEA; 1. PRINTE; PR0011; EGFLAMINTW
InterPro; IPR001791; Laminin G. InterPro; IPR000082; SEA_domain.
                                                                                                                                                                         SMART; SMO0180; EGF Lam; 2.
SMART; SMO0274; FOLN; 2.
SMART; SMO0280; KAZAL; 2.
SMART; SMO0282; LamG; 3.
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| FIGURED | 656 | 716 | NY SIMILARITY | FIGURED | 717 | 718 | NY SIMILARITY | FIGURED | 718 | NY SIMILARITY | FIGURED | 719 | 718 | NY SIMILARITY | 719 | 1111 | 719 | NY SIMILARITY | 719 | 1111 | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 719 | NY SIMILARITY | 71
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GO; GO:0000904; P:cellular morphogenesis during differentiation; IMP.
DR GO; GO:0045193; P:equator specification; IMP.
DR GO; GO:0045193; P:equator specification; IMP.
DR GO; GO:007446; P:inaginal disc of epithelial cell polarity; IMP.
DR GO; GO:0007446; P:inaginal disc of epithelial cell polarity; IMP.
DR GO; GO:0018149; P:protein-protein cross-linking; IPI.
DR InterPro; IPR008126; Cadherin.
DR InterPro; IPR0082126; Cadherin.
DR InterPro; IPR006219; EGF like.
DR InterPro; IPR006219; EGF like.
DR InterPro; IPR006219; EGF like.
DR Pfam; PF00028; Cadherin.
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DR PRART; SM00112; CA; 34.
DR SMART; SM00122; CADHERIN.
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CADHERIN 34.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
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RA MEDINESETABLES

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewer S.E., Holt R.A., Rabburner M., Handerson S.N.,

Barandon R.C., Ragers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Febrankoch C., Baldwin D.,

Ballew M.K.H., Doyle C., Barater E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Barin J. R., Basun A., Barandla J., Bayrattaroglu L., Beasley E.M.,

Ballew K.C., Busam D.A., Bence H., Cadleu E., Center A., Chandra I.,

RA Burris K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burris K.C., Busam D.A., Buller C., Davenport L.B., Davides P.,

RA Cherry J.M., Caally S., Dahle C., Davenport L.B., Davides P.,

RA Goden K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Harris N.L., Evangelista C.C., Ferrar C., Ferrarc S., Pleischman W.,

RA Harris N.L., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibeeyam C.,

RA Harris N.L., Marroy D.A., Heiman T.J., Wei M.-H., Ibeeyam C.,

RA Kimmel B.E., Kodra C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li H.H., Li Leywan C.,

RA Merkulvo G., Milshian N.V., Mobary C., Morris J., Mohrefi A.,

RA Marris S.M., Moy M., Murphy B., Murrphy L., Murny D., Murny D., Murny D., Murny D.,

RA Rainest K., Remington K.A., Nixon K., Nusskern D.R., Parl R.,

RA Shine B.C., Siden-Kiamos I., Simpson M., Stong R., Santh T.,

RA Shine B.C., Siden-Kiamos I., Simpson M., Stong S., Yao Q.A.,

RA Shine B.C., Siden-Kiamos I., Simpson M., Stong S., Yao Q.A.,

RA Shine B.C., Siden-Kiamos I., Simpson M., Stong S., Yao Q.A.,

RA Hang X.H., Zhong F.N., Ribnin G.M., Venter R., Wang S., Yao Q.A.,

RA Hang X.H., Zhong F.N., Ribnin G.M., Venter R., Shin H.,

RA Chene ZB7:2185-2195 (2000).

C. - FUNCTION: Could 
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GO:0008014; F:calcium-dependent cell adhesion molecule ac. . .; NAS.
GO:0016339; P:calcium-dependent cell-cell adhesion; NAS.
GO:0008283; P:cell proliferation; IMP.
                                                       SEQUENCE FROM N.A.

BEDLINES-22069752; PubMed=1959133;
Mahoney P.A., Weber U., Onofrechuk P., Biessmann H., Bryant P.J.,
Goodman C.S.;
"The fat tumor suppressor gene in Drosophila encodes a novel member of the cadherin gene superfamily.";
Cell 67:853-868(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor suppressor. Required for correct morphogenesis.
-- INTIGARITY: Contains 34 cadherin domains.
-- SIMILARITY: Contains 5 EGF-11ke domains.
-- SIMILARITY: Contains 2 laminin G-1ike domains.
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EMBL, AE003577, AAF51036.1; -.
HSSP, P00740, 1EDM.
FlyBase, FBgn0001075, ft.
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Matches 94; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified an institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2), SEQUENCE OF 1122-1129, FUNCTION, SUBGUINT, AND SUBCELLULAR LOCATION.

C. TISSUE=Petal Drain;
X. MEDLINE=99200391; PubMed=10102268;
Bross K., Bland K.S., Mang K.H., Arnott D., Henzel W., Goodman C.S.,
A. Tessier-Lavigne M., Kidd T.;
A. Tessier-Lavigne M., Kidd T.;
Cell 96:795-806(1999).
C. I. FUNCTION: Plays a xrole in axon guidance as a repulsive ligand for ceptors preventing inappropriate midline crossing.
C. I. SUBGRILULAR LOCATION: Secreted. The Cterminal cleavage protein is more diffusible than the larger N-terminal protein that is more tightly cell associated.
C. I. ALTERNATIVE PRODUCTS:
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TISSUE SPECIFICITY: Fetal lung_and kidney, and adult spinal cord.
Weak expression in adult adrenal gland, thyroid, trachea and other
                                                                                                                                                                                                                                                                                        TISSUR=Fetal lung;
MEDLINE=99033071; PubMed=9813312;
Itoh A., Miyabayashi T., Ohno M., Sakano S.;
"Cloning and expressions of three mammalian homologues of Drosophila slit suggest possible roles for slit in the formation and maintenance of the nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissues examined.
--- SIMILARITY: Contains 7 EGF-like domains.
--- SIMILARITY: Contains 23 leucine-rich (LRR) repeats.
--- SIMILARITY: Contains 1 C-terminal cystine knot-like (CTCK) domain.
--- SIMILARITY: Contains 1 C-terminal G-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Distinct but overlapping expression patterns of two vertebrate slit homologs implies functional roles in CNS development and organogenesis.";
                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY.
TISSUE=Fetal brain, and Fetal kidney;
MEDLINE=99279238; PubMed=10349621;
Holmes G.P., Negus K., Burridge L., Raman S., Algar E., Yamada
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=094813-2; Sequence=VSP_050035, VSP_050036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                 094813; 095710; 099597;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Slit homolog 2 protein precursor (h-Slit-2).
Homo sapiens (Human).
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IsoId=094813-1; Sequence=Displayed;
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                                     STANDARD;
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R SMART; SW01019; EGF CA; 2.

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R SMART; SW0019; EGF CA; 2.

R SMART; SW00024; FOLIA; 2...

R SMART; SW00036; LRR TYP; 8.

R SMART; SW00036; LRR TYP; 8.

R SMART; SW00013; LRRNT; 4.

R PROSITE; PS01186; CTCK_1; 1.

R PROSITE; PS01186; CTCK_2; 1.

R PROSITE; PS01186; EGF 2; 7.

R PROSITE; PS01186; EGF 2; 7.

R PROSITE; PS00186; EGF 3; 9.

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R PROSITE; PS00186; EGF 3; 9.

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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
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28-FEB-2003 (Rel. 41, Last sequence update)
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Putative fat-like cadherin-related tumor suppressor homolog
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Score 242; DB 1; Pred. No. 3.9e-09;

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Query Match Best Local Similarity

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A Adame N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adame N.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Adpayani A., An H.-J., Andrews Ffannkoch C., Baldwin D.,
A Abril G.W., Basen A., Baxendale J., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
A Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Dalcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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99VSNB;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Protocodherin-like wing polarity protein stan precursor (Starry night protein) (Flamingo protein).
STAN OR FMI OR CG11895.
                                                                  180 PINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGS-VYIGG--APDVATL
                                                                                                                                                                                                        ----DDGFLAFPGHVFSRSLPEVP
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MEDITNE=99418630; PubMed=10490098;
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polarity under the control of frizzled.";
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     22 CLCRDGFKGDLCEHEEN----PCQLREPCLHGGTCQGTRCLCLPGFSGPRCQQGSGHGI
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the protocadherin family.";
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Bukaryota; Wetazoa; Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                              77 AES-DWHL---EGSGGNDAPGQYGAYFH----
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DOMAIN
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          Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Porler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Rocher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Rad Glodek A., Gong F., Gorrell J.H., G. Guan P., Harris M.,

Harris N.L., Harvey D.A., Heimander J.S., Houck J.,

Rad Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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Mount S.M., Moy M., Murphy B., Murphy L., Mozhed D.D.,

Rad Jazzolo M., Pittman G.S., Pan N.S., Pollard J., Pari V., Reese M.G.,

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Spier E., Spradling A.C., Staplaten M., Strong R., Sun E.,

Spier E., Spradling A.C., Staplaten M., Strong R., Sun E.,

Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Walliams S.M., Woodage T., Woilby K.C., Wu D., Yang S., Yao Q.A.,

K. Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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The genome sequence of Drosophila melanogaster ", "

Rocience 287:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1. SUBCELLULAR LOCATION: Integral membrane protein.
-1. SUBCELLULAR LOCATION: In the pupal wing, expressed at relatively
even levels in all regions. Abundant in 6-9 hour embryos.

EXPLESSED at higher levels in pupae than larvae.

EXPLESSED at higher levels in pupae than larvae.

-1. DEVELOPMENTAL STAGE: At 12 hours after puparium formation (apf),
expressed evenly at cell boundaries. By 30 hours apf, expression
is concentrated at proximal and distal cell boundaries with little
or no expression at anterior and posterior boundaries with little
or no expression at anterior and posterior boundaries. When
prehairs emerge at 30-36 hours apf, expression becomes evenly
distributed again along the whole cell boundary.

-1. SIMILARITY: Contains 8 cadherin domains.

-1. SIMILARITY: Contains 2 laminin G-like domains.

-1. SIMILARITY: Contains 1 GPS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D. N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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GO; GO:0016021; C:integral to membrane; NAS.
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GO; GO:0008014; F:calcium-dependent cell adhesion molecule ac. . .; IMP. RO; GO:0005057; F:receptor signaling protein activity; IMP. GO; GO:001222; P:frizzled morphogenesis; IMP. RO; GO:0007222; P:frizzled signaling pathway; IMP. RO; GO:0007327; P:frizzled signaling pathway; IMP. RO; GO:0007367; P:segment polarity determination; IMP. RITERPRO; IRR002126, Cadherin.

RITERPRO; IRR008895; Canherin.

RITERPRO; IRR008895; Cond. like_lec_gl.

RITERPRO; IRR008895; PORM. receptor.

RITERPRO; IRR008832; GPCR_secretin.

RITERPRO; IRR008832; Morm. receptor.

RITERPRO; IRR008032; Morm. receptor.

RITERPRO; IRR008032; PORM. receptor.

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RITERPRO; IRR008032; PORM. receptor.

RITERPRO; IRR008032; PORM. receptor.

RITERPRO; IRR008033; PORM. receptor.

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DR PROSITE; PSO1022; EGF 1; 4.

DR PROSITE; PSO1026; EGF 2; 3.

DR PROSITE; PSO10649; GFFOTEIN RECEP F2 1; FALSE NEG.

DR PROSITE; PSO0649; G PROTEIN RECEP F2 2; FALSE NEG.

DR PROSITE; PSO2027; G PROTEIN RECEP F2 2; FALSE NEG.

DR PROSITE; PSS0221; GFROTEIN RECEP F2 4; 1.

DR PROSITE; PSS0221; GFR; 1.

DR PROSITE; PSS0221; GFR; 1.

DR PROSITE; PSS0221; GFR; 1.

THE CALCIUM-DINGING REPER RGF; 1.

Cell adhesion; Developmental protein; G-protein coupled receptor; (W Calcium-binding; Repeat; Signal; Transmembrane; EGF-like domain; T SIGNAL 1

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1 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
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CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 7.
CADHERIN 8.
EGF-LIKE 1.
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; PS00232; CADHERIN 1; 6.
;; PS50268; CADHERIN 2; 8.
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Pfam; PF00054; laminin G; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; EGFLAMININ.
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PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00112; CA, B.
SMART; SM00179; EGF. CA, 1.
SMART; SM00303; GPS; 1.
SMART; SM00303; GPS; 1.
PR05ITE; PS00232; CADHERIN 1
PROSITE; PS00232; CADHERIN 1
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1482 EVDLC-YSDPCQNGGTCVRREGGYTCVCPSTHTGQNCETGVGHLRPCPSETCEGGLSCLS 1540
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|LLLYN----GRYNELHDFIALEIHEGHVSFSFSLGDHSERISVIQEAKVSDGKWHQVEVV 1647
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Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
"Human laminin M chain (merosin): complete primary structure,
chromosomal assignment, and expression of the M and A chain in human
fetal tissues."
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDILINE=97066955; PubMed=8910357;
Zhang X., Vuolteenaho R., Tryggvason K.;
Structure of the human laminin alpha2-chain gene (LAMA2), which affected in congenital muscular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P24043; Q14736; Q93022;
01-MR-1992 (Rel. 21, Created)
15-MNOV-1997 (Rel. 35, Last annotation update)
15-MR-2004 (Rel. 45, Last annotation update)
Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
                                                                                                                             Score 225; DB 1; Length 3579;
Pred. No. 4.7e-08;
52; Mismatches 120; Indels 116;
LAMININ G-LIKE 2.
EGF-LIKE 3 CALCIUM-BINDING.
EGF-LIKE 4 CALCIUM-BINDING.
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[3]
SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
                                                                         POLY-HIS.
POLY-ARG.
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Cell Biol. 124:381-394(1994).
                                                                                                                                 14.48;
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LUMAZ_HUMAN
AC P24043
DT 01-NWAN
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DE Lamin)
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GN IAMAZ
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WEDLINE-22439669; PubMed=125256;

RA TEZAK Z. Prandini P., Boscaro M., Marin A., Devaney J., Marino M., REDLINE-22439669; PubMed=125256;

RA FEAR Z. Prandini P., Boscaro M., Marin A., Devaney J., Marino M., Fanin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C., Angelini C., Hoffman E.P., Pegoraro E.;

RT Folinical and molecular study in congenital muscular dystrophy with partial laminin alpha-2 (LAMA2) deficiency.";

RT Full Mutat. 21:103-111(2003).

LI FUNCTION: Binding to cells via a high affinity receptor, laminin of the complex to mediate the attachment, migration and organization of cells into tisques during embryonic development by interacting with other extracellular matrix components.

C. SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to cach othyreptide chains (alpha, beta, gamma), which are bound to cach other by disulfide bonds into a cross-shaped molecule components.

C. SUBUNIT: Laminin is a subunit of laminin-2 (merosin) and laminin-4 (S-merosin).

C. SUBLILIULAR LOCATION: Extracellular; found in the basement membranes (major component subone, stringle persist and some other regions of the brain; not in liver, thymus and bone.

C. TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve, cardiac muscle, panceres, lung, spleen, kinche consent the brain; not in liver, thymus and some other regions of skin, testis, meninges, chrocid placus, and some other regions of skin, testis, meninges, chrocid placus, and some other regions of strin, tother laminin chains to form a coiled coil structure.

C. DOMAIN: Domains VI, IV and G are globular.

C. DOMAIN: Domains VI, IV and G are globular.

C. DOMAINSITY: Contains 1 laminin N-terminal domains.

C. SIMILARITY: Contains 2 laminin W-tike domains.

C. SIMILARITY: Contains 2 laminin GF-like domains.

C. SIMILARITY: Contains 2 laminin GF-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Congenital muscular dystrophy with primary partial laminin alpha-2 chain deficiency: molecular study.";
Neurology 57:1319-1322 (2001).
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VARIANT MDCIA PRO-2564.

BETOINTE-21476611; PubMed=11591858;
He Y., Jones K.J., Vigniar N., Morgan G., Chevallay M., Barois A.,
Estournet-Mathiaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
                                                                                                                                                                                                                                                                                                                       VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614. Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z., Marzluf G.A., Amato A.A., Mendell J.R.; Marzluf G.A., Amato A.A., Mendell J.R.; the laminin 2-chain coding region detected by RNA/SSCP analysis."; Hum. Mutat. 13:174-174(1999).
TISSUE=Placenta;
MEDLINE=90238994; PubMed=2185464;
Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E
"Merosin, a tissue-specific basement membrane protein, is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
Marzluf G.A., Amato A.A., Mendell J.R.;
Hum. Mutat. 13:340-340(1999).
                                                                                                                                                 "Merosin, a tissue-specific basement membrane prolaminin-like protein.";
Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990)
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182 NDGEMHRVTALREGRRGSIQVDGEELVSGRSPQPNVA--VNAKGSVYIGGAP-DVAILIG 238

2843 NDGQWHKIKIMRSKQEGILYVDG---ASNRTISPKKADILDVVGMLYVGGLPINYITRRI 2899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2788 TIELEVRIERAESGLLFYMA----AINHADFATVQLRNGLPYFSYDLGSGDTHTMIPTKI 2842
DR InterPro; IPR008979; Gal bind like.

DR InterPro; IPR002034; Laminin_B.

R InterPro; IPR002049; Laminin_B.

DR InterPro; IPR001791; Laminin_G.

DR Pfam; PP00052; laminin_Br; 2.

DR Pfam; PP00054; laminin_Br; 2.

DR Pfam; PP00054; laminin_G; 5.

DR Pfam; PP00055; laminin_G; 5.

DR Pfam; PP00031; Laminin_B; 1.

DR PROMO11; EGFLAMININ.

DR SMART; SM00180; EGFLami; 15.

DR SMART; SM00281; Lami; 2.

SMART; SM00281; Lami; 2.

DR SMART; SM0022; EGFLiil.

DR PROSITE; PS01186; EGF2; 14.

DR PROSITE; PS01186; EGF2; 3.

DR PROSITE; PS01186; LAMININ TYPE EGF; 14.

DR PROSITE; PS01025; LAMININ TYPE EGF; 14.

DR PROSITE; PS01025; LAMININ TYPE EGF; 14.

DR PROSITE; PS01024; LAMININ TYPE EGF; 14.

DR PROSITE; PS01024; LAMININ TYPE EGF; 14.

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POTENTIAL.
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007310; Q07311; Q07312; Q07313; Q07314;

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neurexin 3-alpha precursor (Neurexin III-alpha).
NRXN3.
RATUS norvegicus (Rat).
Rattus norvegicus (Rat).
Rutharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mucharyota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=55209856; PubMed=7695896; Ullrich B., Ushkaryov Y.A., Suedhof T.C.; C.; Cartography of neuraxins: more than 1000 isoforms generated by alternative splicing and expressed in distinct subsets of neurons."; Neuron 14:497-507(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 223.5; DB 1; Length 3110; 36.4%; Pred. No. 5.1e-08; tive 22; Mismatches 68; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=Sprague-Dawley, TISSUS-Brain;
MEDLINE=93342001; PubMed=8341647;
UShkaryov Y.A., Suedhof T.C.;
"Neurexin III alpha: extensive alternative splicing generates membrane-bound and soluble forms.";
Proc. Natl. Acad. Sci. U.S.A. 90:6410-6414(1993).
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MEDLINE=99074239; PubMed=9856994;
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TISSUE-Brain;
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Matches 59; Conservative
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GO:0005199; F:structural molecule activity; TAS.
GO; GO:0007517; P:mascle development; TAS.
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InterPro; IPR006209; EGF_Like.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                   1 Subunity: The laminin G-like domain 2 binds to neurexophilin 1.

1 Soforms alpha 4B bind to alpha-dystroglycan. The cytoplasmic C-
terminal region binds to CASK.

1 SubcELLUIAR LOCATION: Type In membrane protein (Potential). Some
isoforms seems to be secreted.

1 ALTERNATIVE RROUGTS:

Comment=Alternative splicing; Named isoforms=1;
Comment=At least 288 isoforms may be produced by alternative
splicing: There is a combination of five alternative splicing: There is a combination of five alternative spliced
domains at sites 1, 3, 4 and 5, each consisting of modular
sequences (A-L) that seem to be used independently. Isoforms
Splicing: There is a combination of five alternative spliced
commains at sites 1, 3, 4 and 5, each independently. Isoforms
Splicing: There is a combination of five the transmembrane domain;

1 Salva Alaba JASAASI;
1 Solda-007310-1; Sequence=Displayed;
1 TISSUS SPECIFICITY: Brain.
1 TISSUS SPECIFICITY: Brain.
1 SIMILARITY: Contains 6 laminin G-like domains.
1 SIMILARITY: Belongs to the neurexin family.
                                                                              MEDLINE=9625688; PubMed=8786425;
Hata Y., Butz S., Suedhof T.C.;
"CASK: a novel digle homolog with an N-terminal
calmodulin-dependent protein kinase domain identified by interaction
                                                                                                                                  With neurexins...

J. Neurosci. 16:2488-2494(1996).

[5]

INTERACTION WITH ALPHA-DYSTROGLYCAN.

MEDLINE=21363578; PubMed=11470830;

Sugita S., Saito F., Tang J., Satz J., Campbell K., Suedhof T.C.;

"A scoichiometric complex of neurexins and dystroglycan in brain.";

J. Cell Biol. 154:435-445(2001).

-!- FUNCTION: Neuronal cell surface protein that may be involved in cell recognition and cell adhesion. May mediate intracellular signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO0095; Asx hydroxyl S.

InterPro; IPRO0898; ConA like_lec_gl.

InterPro; IPRO06209; EGF_like.

InterPro; IPRO06210; IEGF_like.

InterPro; IPRO06210; IEGF.

InterPro; IPRO06210; IEGF.

InterPro; IPRO06310; IEGF.

InterPro; IPRO0638; Neurexin-like.

R InterPro; IPRO0698; Neurexin-like.

Pfam; PPO0008; EGF; 3.

R SMART; SM00294; Al.m; 1.

SMART; SM00294; Al.m; 1.

R RART; SM00181; EGF; 3.

R PROSITE; PS00010; ASX HYDROXYL; 1.

R PROSITE; PS00022; EGF-1; FALSE NEG.

R PROSITE; PS00025; EGF-2; FALSE NEG.

R PROSITE; PS00025; Lamd, G DOMAIN; 6.

Signal; Transmembrane; Repeat; Cell adhesion; EGF-like domain; Glycoprotein; Alternative splicing.
 Missler M., Hammer R.E., Suedhof T.C.;
"Neurexophilin binding to alpha-neurexins. A single LNS domain functions as an independently folding ligand-binding unit.";
J. Biol. Chem. 273.14716-34723 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L14851, AAA02857.1; --
EMBL, L14851, AAA02886.1; --
EMBL, L14851, AAA02883.1; --
EMBL, L14851, AAA02853.1; --
EMBL, L14851, AAA02855.1; --
EMBL, L14851, AAA02854.1; --
HSSP, Q63373; IC48.
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INTERACTION WITH CASK
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/FIId=VSP 003525.
Missing (in some isoforms Alpha 4B).
/FIId=VSP 003526.
Missing (in some isoforms Alpha 5B, Alpha 5D, Alpha 5F, Alpha 5H, Alpha 5J and Alpha 5L).
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Missing (In some isoforms Alpha 5A, Alpha
5B, Alpha 5C, Alpha 5B, Alpha 5E, Alpha
5F, Alpha 5G, Alpha 5H, Alpha 5K and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANPTERGIFRVEGASEVIRESNSTIGMVVGIVAAAALCILI
LIYAMYKYRNRDEGSYQVDETRNYISNSAQGSNGTLMKEKQA
SKGGHKKÇKNKOKEYTV -> ARSSNAARIIPCRPYYDMA
THLHIYESHHLLGSTLIDPELPEPRPEPRLPESALIKE
MCCHPPP (in some isoforms Alpha 5A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANFTERDITRY VPGASEVIRESNSTTGMVVGIVAAAALCILI
LLYAMYKYRNRDEGSYQVDETRNYISNSAGSNGTLMKEKQA
SSKSGHKKOKKOKKEYYV -> VLERRIILMIKTNAHPKSL
QSKTC (in some isoforms Alpha 5C and
Alpha 5D)
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ANPTEBGIRSVPGABEVIRESNSTTGMVVGIVAAAALCILI
ANPTEPGIRSVPGABEVIRESNSTISNSAGSNGTLMKEKQA
SSKSGHKKQRNKDKEXYV -> DILLKSF (in some
igoforms Alpha 5E and Alpha 5F);
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LIVAMTKKRRNEGGSYQVDETRNYISNSAQSNGTLMKEKQA
SKSGHKKQKOKKDKEYYV -> ATTTTKKSNFOEGGNSICP
RAPLHNFLL (IN SOME ISOFORMS Alpha SG and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in bom. Alpha ib).
/Fildevsp 003521.
Missing (in some isoforms Alpha iF).
/mrd=vsp_003522.
/mrd=vsp_003522.
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LAMININ G-LIKE 6.
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LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
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                                                                                                                                      LAMININ G-LIKE 1.
                                                                                                                                                                                     LAMININ G-LIKE 2.
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                          NEUREXIN 3-ALPHA
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Pfam; PF01825; GPS; 1
Pfam; PF02793; HRM; 1
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                                                                                                                                                             27 GFKGDLCE-----OGTRCLC--HEBNPCQLREPCLHGGTC----QGTRCLC-LPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIATUR=2033112; PubMed=10907856;
MEDIATUR=2033112; PubMed=10907856;
Vincent J.B., Skaugu J., Scherer S.W.;
"The human homologue of flamingo, EGFL2, encodes a brain-expressed large caddherin-like protein with epidermal growth factor-like domains, and maps to chromosome 1p13.3-p21.1.";
DNA Res. 7:233-235 (2000)
                                                                                                                                                                                                                                               64 SGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPGHVFSRSLPEVPETI
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HCT4; Q92566; 28-141, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last amontation update) Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Epidermal growth factor-like 2) (Multiple epidermal growth factor-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;

MEDLINE=97191544; PubMed=9039502;

MEDLINE=97191544; PubMed=9039502;

Obgase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
Obgase T., Sanaka A., Kotani H., Miyajima N., Nomura N.;

"Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KRAA0201-KIAA0280)

analysis of CDNA clones from cell line KG-1 and brain.";

DNA Res. 3:321-329(1996).

-!- FUNCTION: Receptor that may have an important role in cell/cell signaling during nervous system formation.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Highest expression in brain and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                              48;
                                                                           Ouery Match
Best Local Similarity 26.1%; Pred. No. 1.2e-07;
Matches 73; Conservative 38; Mismatches 121; Indels 4
                      /FTId=VSP 003532.
1578 AA; 173993 MW; 936CF8529143D0C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor genes.", Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 RFSSGITGCVKNLVL--HSARPGAPPQPLDLQHRAQAGA 277
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CELSR2 OR CDHF10 OR EGFL2 OR MEGF3 OR KIAA0279.
  Alpha 5H).
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CC -1- SIMILARIY: Belongs to family 2 of G-process coupled receptors.

CC -1- SIMILARIY: Contrains 9 cafety 2 of G-process coupled receptors.

CC -1- SIMILARIY: Contrains 9 cafety deamins.

CC -1- SIMILARIY: Contrains 9 machine deamins.

CC -1- SIMILARIY: Contrains 8 machine deamins.

CC -1- SIMILARIY: Contrains 8 machine deamins.

CC -1- SIMILARIY: Contrains 8 machine deamins.

CC -1- SIMILARIY: Contrains 9 machine and the machine deamins between the Saysa intellectual coupled deamins.

CC -1- SIMILARIY: Contrains 9 machine and the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins of the machine deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deamins deam
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                                                                                                                                                                                                                                                                       1351 FKCDCPSGDFEKPYCQVTTRSFPAHSFITFRGLRQRFHFTLALSFATKERDGLLLYN--- 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1292 CYSR-PCGPHGRCRSREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCKNGGTCVNLLVGG
                                                                                                                                              1232 CLREPCENYMRCVSVLRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGFTGDYCETEVDL
                                                                                                                                                                                                                                                                                                                                                                                                     1467 QTGLPQGPSEQKVAVVTVDGCDTGVALRFGSVLGNYSCAAQGTQGGSKKSLDLTGPLLLG
                                                                                                                1 CEROPCOHGATCMPAGEYB-------FQCLCRDGFKGDLCEHEENP
                                                                                                                                                                             40 CQLREPCLHGGTCQ----GTRCLCLPGFSGPRCQQG--SGH----GIAESDWH----LEGS
                                                                                                                                                                                                                                          87 GGNDAP-GOYGAYFHDDGFLAFPGHVF--SRSLPE-VPETIELEVRISTASGLLLWQGVE
                                                                                                                                                                                                                                                                                                                                       1408 -GRFNEXHDFVALEVIQEQVQLTFSAGESTTTVSPFVPGGVSDGQWHTVQLKYYNKPLLG
                                                                                                                                                                                                                                                                                                                                                                      190 -TALREG-------RRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIG
                                                                                                                                                                                                                                                                                                         143 VGEAGOGKDFISLGLQDGHLVFRYQLGSGEARLVSEDP--INDGEWHRV-----
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Fast annotation update)
28-FEB-2003 (Rel. 41, Fast annotation update)
CELSR2 OR MEGF3.
                                                                                 91;
   2345 2345 N-LINKED (GLCNAC. .) (POTENTIAL.)
2923 AA; 317447 MW; 382757D315158EDB CRC64;
                                                  Length 2923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||:
| CVPDLPESFPVRMRQ-FVGCMRNLQVDSRHIDMADFIANNGTVPGCP 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                     229 GAPDVATLIGGRFSSGITGCVKNLVLHSAR-------PGAP 262
                                                                                 Indels
                                               13.5%; Score 211.5; DB 1; 23.3%; Pred. No. 3.4e-07; ive 43; Mismatches 132;
                                               Query Match
Best Local Similarity 23.3%
Matches 81; Conservative
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LAMININ G-LIKE 2.
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EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 17, CALCIUM-BINDING.
EGF-LIKE 17, CALCIUM-BINDING.
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R HSSP; P00740; IEDM.

G G0:0004930; F:Greater to membrane; ISS.

GO; G0:0004930; F:Greater coupled receptor activity; ISS.

GO; G0:0004930; F:Greater coupled receptor protein signalin...;

InterPro; IPR000125; Asx hydraxyl S.

InterPro; IPR000125; Asx hydraxyl S.

InterPro; IPR000126; Cadherin.

R InterPro; IPR000189; CanA like lec_gl.

InterPro; IPR001891; BGF Ca.

InterPro; IPR001891; BGF Ca.

InterPro; IPR001893; GCR_escretin.

InterPro; IPR001893; GCR_escretin.

InterPro; IPR001893; GCR_escretin.

InterPro; IPR001894; Laminin EGF.

InterPro; IPR001894; Laminin G.

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EGF-LIKE 2. CALCIUM-BINDING.
EGF-LIKE 3. CALCIUM-BINDING.
LAMININ G-LIKE 1.
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MEDLINE=21818471; PubMed=11829758; MEDLINE=21818471; PubMed=11829758; Garbe J.H., Gohring W., Mann K., Timpl R., Sasaki T.; Complete sequence, recombinant analysis and binding to laminins and sulphated ligands of the N-terminal domains of laminin alpha3B and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 64-281 FROM N.A.
MEDLINE=93179178; PubMed=7874173;
Xu H., Wu X.R., Wewer U.M., Engvall E.;
"Murine muscular dystrophy caused by a mutation in the laminin alpha 2 (Lama2) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING TO FBLN1, FBLN2, AND NID2.
BINDING TO FBLN1, FBLN2, AND NID2.

Talls J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;

"Binding of the G domains of laminin alphal and alpha2 chains and
perflecan to heparin, sulfatides, alpha-dystroglycan and several
extracellular matrix proteins.";

EMBO J. 18:863-870(1999).
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                         "Cloning and expression of laminin alpha 2 chain (M-chain) in the
                                                                                   IMAZ MOUSE STANDARD; PRT; 3106 AA.
Q60675; Q05003; Q64061;
Q1.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 43, Last annotation update)
Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C55BL/6; TISSUE=Thymus;
MEDLINE=93346725; PubMed=8345183;
Chang A.C., WadSworth S., Coligan J.E.;
"Expression of merosin in the thymus and its interaction with
             SEQUENCE FROM N.A.
STAINSFUB/N; TISSUE=Embryo, and Heart;
MEDLINE=$511629; PubMed=7795883;
Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
GAPDVATLTGGRESSGITGCVKNLVLHSAR--------PGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 151:1789-1801(1993).
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 2162-2279 FROM N.A.
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Biochem. J. 362:213-221(2002).
                                                                                                                                                                                                                                                                                                                                                    Matrix Biol. 14:447-455(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genet. 8:297-302(1994).
                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Lama2) gene.
                                                                                                                                                                                                                                                                                                             Yamada Y.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped modecule comprising one long and three short arms with globules at each end. The alpha-2 chain is a subunit of laminin-2 (Merosin) and laminin-4 (S-merosin). Interacts with FBLN1, FBLN2 and NID2. SUBCELLULAR LOCATION: Extracellular. TISSUE SPECIFICITY: Found in the basement membranes (major
                                                                                         DOWAIN: The alpha-helical domains I and II are thought to interact with other laminic chains to form a coiled coil structure. DOMAIN: Domains VI, IV and G are globular.

DISEASE: Defects in LAMA2 are a cause of murine muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAMININ ALPHA-2 CHAIN.
LAMININ N-TERMINAL (DOWAIN VI).
LAMININ BGF-LIKE 1.
LAMININ BGF-LIKE 2.
LAMININ BGF-LIKE 3.
LAMININ BGF-LIKE 4.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 5.
LAMININ BGF-LIKE 6.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 7.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 10.
LAMININ BGF-LIKE 11.
                                                                                                                                                -1- SIMILARITY: Contains 1 laminin N-terminal domain.
-1- SIMILARITY: Contains 17 laminin BGF-like domains.
-1- SIMILARITY: Contains 2 laminin IV domains.
-1- SIMILARITY: Contains 5 laminin G-like domains.
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LAMININ EGF-LIKE 12.
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2784 TIELEVRTEAESGLLFYMG-RINHA----DFGTVQLRNGFPFFSYDLGSGSTRTMIPTKI

NDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVA--VNAKGSVYIGGAP-DVATLTG 238

Search completed: March 9, 2004, 17:19:44 Job time: 7.86906 secs.

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Ogoty5 rattus norv
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Logicance of 1-153 From N.A.

Denzer A.J., Brandenberger R., Gesemann M., Chiquet M., Ruegg M.A.;
J. Cell Biol. 0:0-0(0).

EMBL; AF016903; AA5229176.1;

EMBL; OR4406; AA552917.1;

ENBL; D00740; IEDM.
Genew; HGCC:329; AGRN.
GO: GO: 0005198; F: structural molecule activity; IEA.
InterPro; IPR004850; Agrin NtA.
InterPro; IPR006209; EGF 11ke.
InterPro; IPR005209; EGF 11ke.
InterPro; IPR005209; EGF 11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUJ-1997 (TrEMBLrel. 04, Created)
01-JUJ-1997 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
AGRIN precursor (Fragment).
Homo sapiens (Human).
Homo sapiens (Traman).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-153 FROM N.A.
MEDLINE=96224170; PubMed=8617505;
Lennon G., Auffray C., Polymeropoulos M., Soares M.B.,;
"The I.M.A.G.E. Consortium: an integrated molecular analysis of genomics and their expression.";
Genomics 33:151-152(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] —
SEQUENCE FROM N.A.
Groffen A.J.A., Buskens C.A.F., Van Kuppevelt T.H.M.S.M., Veerkamp J.H., Monnens L.A.H., van den Heuvel L.P.W.J.;
Eur. J. Biochem. 0:0-0(1998).
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QBNZV8
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InterPro; IPR002350; Kazal.
InterPro; IPR002049; Laminin EGF
InterPro; IPR001791; Laminin G
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2280.5
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Q90768 caenorhabdi
Q90761c1 homo sapien
Q8n312 homo sapien
Q8n370 homo sapien
Q800x4 mus musculu
Q80953 mus musculu
Q89544 mus musculu
Q8714 farosophila
Q9774 drosophila
Q90714 homo sapien
Q9117 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  000468 homo sapien
Q9u7e8 caenorhabdi
                                                                       March 9, 2004, 17:15:08 ; Search time 24:8707 Seconds (without alignments) 3602.917 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                           1 CEROPCOHGATCMPAGEYEF........OPLDLOHRAQAGANTRPCPS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                 OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q961C1
Q8NAL2
Q8NYO
Q80WX4
Q90WX4
Q99KT4
Q8K326
Q96K3D6
Q96K3D6
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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sp_bacteria:*
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Database

088279 rattus norv

Result No.

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263 PPOPLDLOHRAQAGANTRPC 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1593 QCECPLGREGTRCQTAS-------GODGSGPFLADFNGFSHLELRGLHTFAR 1637
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MEDLINE=99443780; PubMed=10512861;
MULLE G.P., Rogalski T.M., Bush J.A., Gorji P.R., Moerman D.G.;
Moorplex patterns of alternative splicing mediate the spatial and
temporal distribution of Perlecan/UNC-52 in caenorhabditis elegans.";
Mol. Biol. Cell 10:3205-3221(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 22.8%; Score 357.5; DB 4; Length 2026; Local Similarity 35.4%; Pred. No. 4.7e-19; Los 91; Conservative 29; Mismatches 110; Indels 27; Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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2026 AA; 212881 MW; 4ABOEE710CD4B8EF CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
UNC-52/perlecan (Fragment).
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF 1; 6.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01249; LAMINIM TYPE EGF; 1.
PROSITE; PS50024; SEA; 1.
PROSITE; PS50024; SEA; 1.
PROSITE; PS01148; UPF0033; 1.
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                                                             Pfam; PF00008; EGF; 4.
Pfam; PF00050; kazal; 9.
Pfam; PF00053; laminin EGF; 2.
Pfam; PF00154; laminin G; 3.
Pfam; PF01150; SEA; 1.
IPR000082; SEA domain.
IPR008993; TIMP like.
IPR001455; UPF0033.
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                                                                                                                                                                                                                          SMART; SM00180;
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SMART; SM00280;
SMART; SM00282;
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Ogenci;

Ol-DEC-2001 (TrEMBLrel. 19, Last sequence update)

Ol-DEC-2001 (TrEMBLrel. 25, Last sequence update)

Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein (Fragment).

Hymo sapiens (Human).

Enkaryota; Metazoa; Cordata; Craniata; Vertebrata; Euther Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 22.3%; Score 349; DB 5; Length 92 Local Similarity 31.2%; Pred. No. 8.1e-19; Local 81; Conservative 41; Mismatches 102; Indels
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EMBL, AF132883; AAD25092.1; -.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-2.
Ffam; PF00064; Igf; 1.
Ffam; PF00064; Igf; 1.
SMART; SM00181; EGF; 3.
SMART; SM00181; EGF; 3.
SMART; SM00181; EGF; 3.
FR05ITE; PS00022; EGF, 1; 3.
FR05ITE; PS00022; IGM, GDOMAIN; 3.
EGF-like domain; Immunoglobulin domain.
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Tasus—Tasus—Tasus—Takemoto M., Sugiyama T., Irie R.,

Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

Kawatami B., Sugiyama A., Takemoto J., Isono Y.,

Rada Hilo Y., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

Rada Hilo Y., Sato K., Washikawa T., Kimura K., Yamashira H.,

Murakawa K., Kanahori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,

Rada Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Rubo human cDNA sequencing project ".,

Submitted (UTL-2002) to the EMBL/GenBank/DDBJ databases.

ENBL, AKO97549; BAC05096.1; -

ENBL, AKO97549; BAC05096.1; -

ENBL, AKO97549; ConA like_lec_gl.

BR InterPro; IPR001881; EGF Ca.

InterPro; IPR001881; EGF Ca.

InterPro; IPR001791; Laminin_G.

BR InterPro; IPR001791; Laminin_G.

BR Ffam; PP00018; EGF 2.

BR SWART; SM0018; EGF 2.

BR SWART; SM0018; EGF 2.

BR RNSITE; PS00022; EGF 1; 3.

BR RNSITE; PS00025; LAM G DOWAN; GlAB1294F0204ED2 CRC64;

SEUENCE 775 AA; 84800 MW; GlAB1294F0204ED2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 DAP----GOYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
                                                                                                                                            90 DAP----GQYGAYFHDDGFLAFPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVEVGE 145
                                                                                                                                                                                                                                                                       146 ACQCKDFISLGLQDGHLVFRYQLGSGEARLVSEDPINDGEWHRVTALREGRRGSIQVDGE 205
                                                                                                                                                                                                                                                                                                                   206 ELVSGRSPGPNVAVNAKGSVYIGGAPDVATLIGGRFSSGITGCVKNLVLHSARPGAPPPQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                    282 EIPQFIGRSYLTYDNPDILKRVSG---SRS----NVFWRFKTTAKDGLLLWRG--DSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Local Similarity 33.5%; Pred. No. 1.9e-18;
Les 86; Conservative 34; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBN7YO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotheital protein FLJ40230.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 PLDLQHRAQAGANTRPC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 HISLVEDAVDGKNINTC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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TISSUE=Testis;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 PINDGEWHRVTALREGRRGSIQVDGEELVSGRSPGPNVAVNAKGSVYIGGAPDVATLT-G 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PGFSGPRCQQGSGHGIAESDWHLEGSGGNDAPGQYGAYFHDDGFLAFPG-HVFSRSLPEV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 LGREGIFCÓTAS------GODGSGPFLADFNGFSHLELRGLHTFARDLGE- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PETIELEVRISTASGLILIMOGVEVGEAGOGKDFISLGLQDGHLVFRYQLGSGEARLVSED 179
                                                                                                                                                                                                                                                                                                                                                  1 CHGGAPCONLEAGRFHCOCPPGRVGPTCADEKSPCQ-PNPCHGAAPCRVLPEGGAQCECP 59
                                                                                                                                                                                                                                                                                           6 COHGAICMPAGEYEFQCLCRDGFKGDLCEHEENPCQLREPCLHGGTCQ-----GTRCLCL 60
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                                                                                                                                                                                                                       27; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                             DB 4; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%; Score 343; DB 4; Length 463; 33.5%; Pred. No. 9.9e-19; ive 34; Mismatches 97; Indels
                                                                                                                                                         Query Match
22.1%; Score 346.5; DB 4; Length 4
Best Local Similarity 35.3%; Pred. No. 5.6e-19;
Matches 89; Conservative 29; Mismatches 107; Indels
                                                                                            488 AA; 51764 MW; A732B99CC680E772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ35160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 AA
PROSITE; PS50025; LAM G DOMAIN; 2.
Hypothetical protein; EGF-like domain.
NON TER
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Best Local Similarity
Matches 86; Conserv
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TISSUE=Placenta;
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                                                                                            SEQUENCE
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Gaps